Modifying the control of gene expression behavior by the deletion of connectrons and by the design and addition of synthetic connectrons in prokaryotic, archea and eukaryotic genomes

Reference to Related Application

The present application includes the subject of Provisional Application Serial No. 60/393,558 filed July 5, 2002

The present application is a continuation in part of US Patent Application Serial Number 09/866,925 filed May 30, 2001 entitled ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

The present application is also related to US Patent Application Serial Number 10/339,666 filed January 10, 2003 entitled SIMULATION OF GENE EXPRESSION CONTROL USING CONNECTRONS, INTERFERENCE RNAS (IRNAS) AND SMALL TEMPORAL RNAS (STRNAS) IN PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

The present application is also related to US Patent Application Serial Number 10/364,516 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE ESCHERICHIA COLI K-12 MG1655 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/364,412 filed February 12, 2003 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE SACCHAROMYCES CEREVISIAE

5   COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/299,056 filed November 19, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE

10   EXPRESSION OF SETS OF GENES IN THE HALOBACTERIUM SP. NRC-1 COMPLETE GENOME

The present application is also related to US Patent Application Serial Number 10/367,832 filed February 19, 2003 entitled

15   DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE PSEUDOMONAS AERUGINOSA PA01, COMPLETE GENOME

The present application is also related to US Patent Application

20   Serial Number 10/287,818 filed November 5, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE VIBRIO CHOLERAE CHROMOSOME I, COMPLETE CHROMOSOME

25   The present application is also related to US Patent Application Serial Number 10/305,275 filed November 27, 2002 entitled DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE EXPRESSION OF SETS OF GENES IN THE AEROPYRUM PERNIX K1 COMPLETE GENOME

30

Introduction

The connectron structure of a genome determines sets of four DNA
sequences of minimum length of 15-bases (C1 and C2 which are in
the 3'UTR of a gene, T1 which is on the 5'-side and T2 which is
5   on the 3'-side of a set of genes). The connectrons in a genome
control the expression of sets of genes. Each native genome has
a particular set of connectrons that control the expression of
sets of genes in many different ways. The gene expression
behavior can be changed by deleting existing connectrons and by
10   adding new connectrons that have been designed to achieve
specific new gene expression patterns. This patent application
describes the invention of methods for deleting connectrons as
well as the invention of four classes of synthetic and designed
connectrons that can be used to modify the connectron behavior
15   of a genome. In addition this application describes the
invention of four methods that implement synthetic connectrons
with differing proportions of novelty.

Definitions

20

Double stranded DNA – Watson and Crick showed in 1953 that DNA
naturally forms a double-stranded helix. A typical double
stranded sequence is

25   5'-TAGAGGAGTACCAC-3'
     3'-ATCTCCTCATGGTG-5'

Hydrogen Bond – The force between a hydrogen atom and another heavier atom such as Oxygen (O), Nitrogen (N), Phosphorus (P), or Sulfur (S).

5   **Positive strand** – The positive strand is normally represented 5' to 3' running left to right as in

5'-TAGAGGAGTACCAC-3'

10 **Negative strand** – The negative strand is normally represented 5' to 3' running right to left as in

3'-ATCTCCTCATGGTG-5'

15 **Single stranded RNA** – Either the positive or the negative strand of the double-stranded DNA can be transcribed by the polymerase. In RNA U replaces T.

RNA of positive strand sequence   5'-UAGAGGAGUACCAC-3'
20 RNA of negative strand sequence   5'-GUGGUACUCCUCUA-3'

Antisense RNA – The antisense strand of any RNA sequence is the complement sequence

25 RNA sequence   5'-UAGAGGAGUACCAC-3'
    Antisense RNA sequence   3'-AUCUCCUCAUGGUG-5'

Triple Strand Helix – The RNA sequence of a RNA/DNA triple-strand complex is the same as the positive strand of the DNA

30
    DNA positive strand   5'-TAGAGGAGTACCAC-3'
    DNA negative strand   3'-ATCTCCTCATGGTG-5'

4

RNA strand   5'-UAGAGGAGUACCAC-3'

Promoter – Any region of DNA, that binds proteins which engage the polymerase transcription mechanism.

5

TATA Box – A region near the 3' end of a promoter with the sequence TATA.

mRNA – The RNA produced from the DNA by the polymerase as a

10   result of transcription

Start of transcription – The 3' end of a promoter where the polymerase mechanism begins to transcribe DNA into mRNA.

15   **Exon** – Any region of mRNA which is used to code for proteins

Intron – Any region of mRNA lying between two exons which is not used to code for proteins. The introns are edited out of the initial RNA transcript to form the mature mRNA.

20

3' UTR – The untranslated 3' end of an mRNA is beyond the end of the last exon. A stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

25   **End of translation** – The 3' end of the 3'-most exon.

Translated region – Any collection of exons and introns.

Gene – Any DNA region that codes for a protein. Introns do not

30   occur in prokaryotic genes and they sometime fail to occur in eukaryotic genes. A typical model of a gene is

```
|<-----Promoter------>|
        |<-TATA Box->|
                       |<-Beginning of Translation
                       |←-----------Translated Region---------------->|
                                                      End of Translation->|
|<-Exon->|<-Intron->|<-Exon->|<-Intron->|<-Exon->|<-3'UTR->|
+ strand ----------------------------------------------------------------
- strand ----------------------------------------------------------------

|<------------------------------Gene------------------------------->|
```

Positive strand gene – Any gene in which the features run 5′ to 3′ on the positive strand

Negative strand gene – Any gene in which the features run 5′ to 3′ on the negative strand

C1 sequence – Any positive or negative strand DNA sequence of 15 bases or more. The C2 sequence must occur in the same chromosome as the C1 sequence.

C2 sequence – Any positive or negative strand DNA sequence of 15 bases or more. The C1 sequence must occur in the same chromosome as the C2 sequence.

C1/C2 – Any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence

T1 sequence – Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T2 sequence. The T1 and T2 sequences must be between about 1kb and 105kb apart.

T2 sequence – Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T1 sequence. The T2 and T1 sequences must be between about 1kb and 105kb apart.

5

Last exon gap or **Gap-Distance** – The number of bases between the end of transcription and the beginning of the C1/C2 sequence. In prokaryotes and single-celled eukaryotes this gap can range from no bases to 500 bases. In multi-celled eukaryotes the gap

10   can be as large as 10,000 bases.

Poly-adenylation signal – A number of Adenosine (A) bases are added to the mRNA at the end of the 3'UTR.

15   **Possible Connectron** – Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the

20   3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences. A triple-stranded complex of the DNA and the RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2

25   sequence. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between about 1kb and 105kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry

30   chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Real Connectron – Any Possible Connectron which is within the Gap-Distance of some gene

Homologous connectron – The T1 sequence and the T2 sequence are on the same chromosome as the C1/C2 sequence

Heterologous connectron – The T1 sequence and the T2 sequence are on a chromosome different from chromosome of the C1/C2 sequence

Permanent connectron – Any C1/C2 sequence, which is 3' UTR to some gene that is not surrounded by any T1 and T2 sequence pairs

Transient connectron – Any C1/C2 sequence, which is 3' UTR to some gene that is surrounded by one or more T1 and T2 sequence pairs

One-shot or Self-limiting connectron – Any C1/C2 sequence which is 3'UTR to some gene that is surrounded by the T1 and T2 sequences such that C1=T1 and C2=T2

Geneless connectron – Any C1/C2 sequence that is not 3'UTR to some gene but is surrounded by some T1 and T2. A promoter may lie 5' to the C1/C2 sequence.

Bi-directionality of Connectron Excitation – A C1/C2 short loop on one strand selects a T1-T2 long loop pair on the same or the opposite strand. The C1/C2 short loop has a complementary C1'/C2' sequence on the opposite strand. Similarly the T1-T2 long loop pair has a complementary long loop pair T1'-T2'. Wherever a C1/C2, T1-T2 tetrad exists there is a complementary C1'/C2', T1'-T2' tetrad. The C1/C2 short loop can be

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transcribed as a 3'UTR to a gene on the same strand. The
C1'/C2' short loop which is on the strand opposite to the C1/C2
short loop can also can be transcribed as a 3'UTR to a gene on
the same strand. There are four possible models of action

5

```
              T1              T2           gene - C1/C2
+ strand ----------------------------------------------------------------
- strand ----------------------------------------------------------------
```

10

```
               T1             T2
+ strand ----------------------------------------------------------------
- strand ----------------------------------------------------------------
                                           C2/C1 - gene
```

15

```
+ strand ----------------------------------------------------------------
- strand ----------------------------------------------------------------
              T2'             T1'          C2'/C1' - gene
```

20

```
                                     gene - C1'/C2'
+ strand ----------------------------------------------------------------
- strand ----------------------------------------------------------------
              T2'             T1'
```
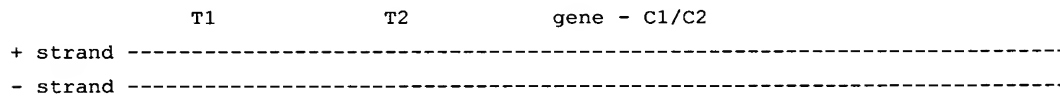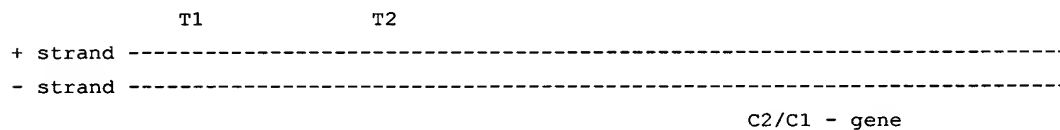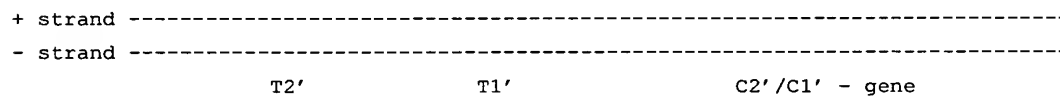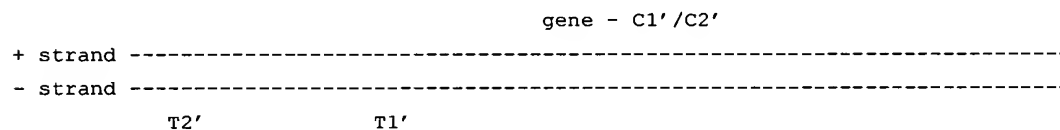
25

Of course, the short loops and the long loops do not have to be
on the same chromosome.

Hierarchy of connectron action – When a C1/C2 is expressed it

30 forms a T1-T2 loop by forming a connectron. The C1/C2 sequence
does not have to be on the same chromosome as the T1 and T2
sequences. This provides a way of causing interaction between
chromosomes. When the T1-T2 loop forms, any genes in that loop
region which had been expressing C1/C2 sequences in their

35 3'UTRs, now cease expressing the C1/C2 sequences. The
connectrons formed by these C1/C2 sequences will cease to exist
after some time thus opening up the genes inside the respective
T1-T2 loops to expression. The hierarchy of connectron action

9

is alternates between repression and expression. The connectron hierarchies can be of any depth.

One-to-Many connectron action – One C1/C2 sequence can form connectrons in many different places on many different chromosomes. The only requirement is that C1=T1 and C2=T2. This makes it possible for one expression event to control the expression of many genes on different chromosomes.

Many-to-One connectron action – C1/C2s that come from many different places on many different chromosomes can form a connectron for a specific T1-T2 sequence pair. The only requirement is that C1=T1 and C2=T2. This makes it possible for many different expression events to control the expression of one set of genes on a particular chromosome.

Many-to-Many connectron action – The arrangement of C1/C2s and T1-T2s across chromosomes can form a complex web of gene expression control relationships.

Percentage of the Genome Regulated by Connectrons – Since the connectrons for a sequenced genome can be calculated, the percentage of the genome that is open to connectron regulation can be known.

Emergent Property – The network of connectrons in any genome emerges from a knowledge of the complete DNA sequence of the genome. Because both the C1/C2 sequences and the T1-T2 sequences can be any place in the genome, the whole genomic sequence must be known before all the connectrons can be determined.

10

Paradigm Shift – For the past fifty years since the discovery by Watson and Crick of the double-helical nature of DNA, the reigning paradigm for scientific discovery has been the study of one gene and its effects on the behavior of a cell. The advent

5   of genomic sequencing and this invention of connectrons that emerge from the whole genome will produce a shift in the way scientists view biological systems and the way they formulate and execute experiments. The many-to-many relationships between the connectrons mean that there are many ways in which the

10   expression of a set of genes can be modulated. The multiplicity of control pathways produces a system stability that makes it possible for biological systems to be stable for long periods of evolutionary time. The thinking that goes into formulating scientific experiments will have to change to accommodate the

15   changes in understanding that will be induced by the application and extension of this patent application.

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20   **Sequence Element** – The double-stranded sequence of either a C1, a C2, a T1 or a T2 of some connectron.

Native Sequence Element – Any sequence element of a connectron which is a constitutive part of the native genome.

25

Native Connectron – Any connectron in which all four (i.e. the C1, C2, T1 and T2 sequence) sequence elements are constitutive parts of the native genome.

30   **Synthetic Sequence Element** – Any sequence element that has been added into a genome at some particular place. The actual sequence of bases may occur in one or more places in the genome.

The synthetic aspect is that an instance has been placed into the genome at a specific place by design.

Copied Sequence Element – Any sequence element that has been
5 copied from one place in a genome to another place in that genome.

Unique Sequence Element – Any double-stranded DNA sequence element for which there is only one pair of instances. Such a
10 pair of instances can be used to implement the C1 and T1 synthetic sequence elements of a connectron or the C2 and T2 synthetic sequence elements of a connectron.

Extracted Sequence – Any sequence element that is moved from one
15 place in a genome to another place in the same genome. The moved sequence element can be unique or non-unique.

Synthetic Connectron – Any connectron in which one or more of the sequence elements in a native connectron are substituted by
20 synthetic sequence elements.

Designed Connectron – Any connectron that does not exist in the native genome.

25 **RNA-Based Connectron** – Any connectron in which the C1 and C2 elements are generated as RNA in the 3'UTR of some gene.

DBP – A multi-domain zinc-finger DNA Binding Protein that binds to a specific DNA double-stranded sequence.
30

Protein-Based Synthetic Connectron – Any synthetic connectron in which the C1 and C2 elements are generated by a DBP.

12

PNA – A Peptide Nucleic Acid is a molecular construct patented and supplied by Boehringer-Mannheim. The A, T, G, C base portions of are the same as an RNA but the ribose ring has been
5   replaced by a peptide-like configuration of atoms.

PNA-Based Synthetic Connectron – Any synthetic connectron in which the C1 and C2 elements are generated by a sequence of Peptide Nucleic Acid (PNA) bases.
10

Generalized Synthetic Connectron – Any synthetic connectron in which the C1 and C2 elements are generated by two linked double-strand DNA binding elements.

15   **Individual Connectron State** – A binary representation of whether the C1-C2 elements are bound to the cognate T1 and T2 elements. A **0** means that the connectron is not formed. A **1** means that the connectron is formed and hence the expression of the genes between the T1 and T2 elements are turned off.
20

Genomic Connectron State – The collection of all the individual native and synthetic connectron states in a genome. The individual connectron states are ordered along each chromosome and plasmid by the position of the T1 element.
25

Connectron Simulation – The temporal transitions of the genomic connectron states as the individual connectron states interact with each other.

13

Content of the CD

The Sequence Listing Part is incorporated herein by reference.
The material contained on this compact disc attached hereto was
5   created on 6/30/03,

synthetic.sequences has 13,770 bytes

Brief Description of the Objects of the Invention

The basic methods patent application provides the methods for determining the structure of the native connectrons in a variety of genomes. Since the original conceptualization of connectrons followed from the work that we did on the design of zinc-finger DNA Binding Proteins (DBPs), US Patent 6,205,404, it has always been the applicant's intention to use these designed proteins to modify genomic connectron behavior.

An object of this invention is to provide a method for utilizing the genomic simulation of connectron behavior to facilitate the optimization of design decisions related to deleting connectrons from a genome or adding connectrons to a genome.

An object of this invention is to provide a method for utilizing the genomic simulation by computer of connectron behavior to facilitate the optimization by computer of design decisions related to deleting connectrons from a genome or adding connectrons to a genome.

An object of this invention is to provide a method for modifying the connectron behavior of a genome by deleting and adding connectrons.

An object of the invention is to provide a method for creating new connectrons in a genome by copying one or more double-stranded DNA sequence elements from one place in the genome to another place in the genome or by extracting a double-stranded DNA sequence element from one place in the genome and moving it

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to another place in the genome or by introducing a new unique pair of double-stranded DNA sequence elements into the genome at specific places.

5   An object of the invention if to provide a method for creating new connectrons in a genome by copying, extracting or adding unique DNA elements in addition to using either DBPs, PNAs or a linked pair of generalized DNA binding elements to implement the C1 and C2 elements of the new connectron.

10

Description of the Tables

Table 1 - The 10 possible ways of deleting a connectron

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Table 2 - The 15 possible synthetic connectrons defined by combinations of native and synthetic elements

Table 3 - The 4 possible synthetic connectrons defined by
10   combinations of native and synthetic DNA elements and synthetic DBP elements

Table 4 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and synthetic
15   PNA elements

Table 5 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and a pair of linked double-strand DNA binding elements
20

Table 6 - The 2 possible ways of implementing a single synthetic element in a synthetic connectron

Table 7 - The 14 possible ways of implementing a pair of
25   synthetic elements in a synthetic connectron

Table 8 - The 41 possible ways of implementing three synthetic elements in a synthetic connectron

30   Table 9 - The 25 possible ways of implementing four synthetic elements in a synthetic connectron

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Description of the Invention

The simulation of the connectron behavior of a genome provides a powerful way of understanding how individual connectrons interact with each other. From the more than 100 genomes whose connectron structure we have determined, it is clear that a given C1-C2 may generate many different connectrons - the one-to-many conectron action mode. Similarly it is clear that a given connectron may be generated by the expression of many different instances of the C1-C2 signal - the many-to-one connectron action mode. The temporal interaction of these one-to-many and many-to-one modes of connectron control of gene expression can best be understood by doing a genomic connectron simulation and looking at the results. This is especially important when determining when and where to delete connectrons from a native genome or add new connectrons to a native genome. Genomic connectron simulation is the subject of a related patent application.

Although there are instances in different genomes of a C1-C2 generating only one connectron, much more frequently a given C1-C2 will generate several connectrons. When only one connectron is generated by a given C1-C2, a decision to delete the connectron or to add another connectron using the same or different C1 or C2 elements will have no side effects as long as the T1 and T2 elements are only used by this connectron. This is the relative infrequent example of one-to-one. Much more frequently, deleting or changing a given C1 or C2 may have multiple consequences and serious behavioral side effects. Modification of genomic connectron control of gene expression will inevitably involve compromises, design decisions, and -

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worst of all – patch-ups. Consider an example in which a given C1-C2 generates two connectrons. For some reason we desire to delete one of the two connectrons. A patch-up can be achieved by finding some other way to generate the second connectron.

5   This could be achieved by adding one or more synthetic connectron elements to generate the second connectron as a synthetic connectron.

If there are no side effects of a design decision then that is
10   the optimum. If there are side effects, the genomic simulation of connectron behavior makes it possible to evaluate the genomic behavioral consequences of the design and implementation decisions.

15   The deletion of a connectron as shown in table 1 can occur in 10 different ways ranging from deleting or modifying just one sequence element to deleting or modifying all four sequence elements. Anything that destroys the sequence recognition of the T1 by the C1 or the T2 by the C2 will have the effect of
20   deleting the connectron.

Any or all of the four elements (C1, C2, T1 and T2) of a native connectron can be replaced with synthetic elements to form a synthetic connectron. Table 2 gives the 15 possible types of
25   synthetic connectrons. A designed connectron can be introduced into a genome to either (1) control the expression of a set of genes already controlled by other native connectrons, or (2) control the expression of a newly selected set of genes. Using DNA sequences, a designed connectron be made from any of the 15
30   combinations of native and synthetic elements in Table 2. If the C1 and C2 elements of a connectron are generated by a zinc-finger DBP then the 4 combinations of synthetic and designed

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connectrons in table 3 are possible. If the C1 and C2 elements
of a connectron are generated by a PNA then the 4 combinations
of synthetic and designed connectrons in table 4 are possible.
If the C1 and C2 elements of a connectron are generated by a
5   linked pair of DNA binding elements then the 4 combinations of
synthetic and designed connectrons in table 5 are possible. The
DNA binding elements G1 and G2 can be proteins or any other
molecular material that recognizes the DNA sequences of the T1
and T2 elements.
10

The implementation of the synthetic elements of a designed
connectron can be achieved in several different ways. In table
2 from one to four of the sequence elements of a connectron can
be substituted by a synthetic sequence element. There are three
15   different ways of creating a synthetic sequence element. An
existing sequence element somewhere in the genome can be copied
into a new location. An existing sequence element can be
extracted from one location in the genome and placed in another
position in the genome. A new pair of sequence elements not
20   otherwise present in the genome can be created. One instance of
this new, unique sequence element must be a C1 or a C2. If the
first instance is a C1 then the second instance of this new,
unique sequence element must be a T1. Similarly, if the first
instance is a C2 then the second instance of this new, unique
25   sequence element must be a T2. Table 6 shows that there are
only two ways of generating a synthetic connectron when only one
synthetic sequence element is used. Implementing a new, unique
sequence element is not possible because these sequence elements
must come in pairs. Table 7 shows that there are 14 ways of
30   implementing a pair of synthetic sequence elements to form a
synthetic connectron. Table 8 shows that there are 41 ways of
implementing three synthetic sequence elements to form a

synthetic connectron. Table 9 shows that there are 25 ways of implementing four synthetic sequence elements to form a synthetic connectron.

Examples

Tables 1 thru 9 provide a large combinatorial number of ways of deleting connectrons from a genome and of adding connectrons to a genome. We give one example of deleting one connectron from a single genome and five examples of a connectron to four different genomes. It is clear that many other variations would be obvious to someone skilled in the art.

Deletion of a Transient Connectron from one chromosome to itself

Connectron 13 is an example of a transient connectron in the *S. cerevisiae* genome. As per table 1, this connectron can be deleted by either deleting or modifying any one or all four of the connectron elements. The C1 and the C2 identifiers are 36 while the T1 identifier is 39 and the T2 identifier is 111. When this connectron is deleted, all the properties stated below disappear.

The original connectron 13 is described as

		C1/C2			T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
13	1	36	36	1	39	111	transient

The C1/C2 source of the transient connectron 13 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
CPT	36	1	1	12.572	12.788	.217	OS->	|||||||||||||||||||||||

22

The "Type" descriptor of this transient C1/C2 connectron source
is "CPT". The letter "P" indicates that the C1/C2 connectron
source occurs on the positive strand of the double-stranded DNA
of the genome. The letter "N" in this place would indicate a
5   C1/C2 connectron source on the negative strand of the genomic
DNA. The letter "T" in this descriptor indicates a "transient"
connectron. Similarly, the letter "P" would indicate a
permanent connectron that is shown in a later example. The
"Start", "Stop" and "Length" descriptors throughout these
10 examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 13 as shown in
table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TP	39	1	1	12.572	12.807	.236	*-++++++++++++++++++*
TN	40	8	1	12.908	12.964	.057	*-++++++++++++++++++*
CNT	41	1	1	12.908	12.964	.057	--> ||||||||||||||||||||
CPT	42	1	1	12.908	12.964	.057	--> ||||||||||||||||||||
TP	43	1	1	12.922	12.964	.043	*-++++++++++++++++++*
CNT	44	1	1	12.966	12.986	.021	--> ||||||||||||||||||||
CPT	45	8	1	12.966	12.986	.021	--> ||||||||||||||||||||
TP	46	1	1	12.966	12.986	.021	*-++++++++++++++++++*
TN	47	1	1	13.027	13.159	.133	*-+++++++++++++++++++++*
CNT	48	1	1	13.028	13.099	.072	OS-> ||||||||||||||||||||||||
TP	49	1	1	13.028	13.099	.072	*-+++++++++++++++++++++*
CPT	50	1	1	13.053	13.124	.072	OS-> ||||||||||||||||||||||||
TP	51	1	1	13.102	13.159	.058	*-+++++++++++++++++++++*
CNT	52	1	1	13.105	13.246	.142	--> ||||||||||||||||||||||||
CPT	53	1	1	13.130	13.246	.117	--> ||||||||||||||||||||||||
TN	54	1	1	13.176	13.194	.019	*-++++++++++++++++++++++++*
TN	55	1	1	13.196	13.231	.036	*-++++++++++++++++++++++++**
TP	56	1	1	13.211	13.246	.036	*-+++++++++++++++++++++++++++
CPT	57	1	1	13.253	13.290	.038	--> ||||||||||||||||||||||||||
TN	58	1	1	13.253	13.290	.038	*-+++++++++++++++++++++++++++
TP	59	1	1	13.255	13.285	.031	*-+++++++++++++++++++++++++++
CNT	60	1	1	13.255	13.290	.036	--> ||||||||||||||||||||||||||
CPT	61	8	1	13.295	13.315	.021	--> ||||||||||||||||||||||||||
TN	62	8	1	13.295	13.317	.023	*-+++++++++++++++++++++++++++
CNT	63	8	1	13.340	13.379	.040	--> |||||||||||||||||||||||||||
CPT	64	8	1	13.341	13.380	.040	--> |||||||||||||||||||||||||||

23

```
     GG    65   1  1   13.364   13.744   .381 Group0004  |||||||||||||||||||||||||||||||
     CPT   66   1  1   13.387   13.405   .019       -->  ||||||||||||||||||||||||||||||
     TN    67   8  1   13.387   13.413   .027       *-+++++++++++++++++++++++++++++++
     TP    68   1  1   13.444   13.460   .017       *-+++++++++++++++++++++++++++++++
  5  CPT   69   8  1   13.566   13.582   .017       -->  ||||||||||||||||||||||||||||||
     TN    70   8  1   13.574   13.591   .018       *-+++++++++++++++++++++++++++++++
     CPT   71   8  1   13.585   13.599   .016       -->  ||||||||||||||||||||||||||||||
     TN    72   1  1   13.656   13.681   .026       *-+++++++++++++++++++++++++++++++
     TP    73   1  1   13.656   13.706   .051       *-+++++++++++++++++++++++++++++++
 10  TN    74   9  1   13.704   13.726   .023       *-+++++++++++++++++++++++++++++++
     CPT   75   1  1   13.709   13.726   .018       -->  ||||||||||||||||||||||||||||||
     TN    76   1  1   13.734   13.750   .017       *-+++++++++++++++++++++++++++++++
     CPT   77   1  1   13.734   13.782   .049       -->  ||||||||||||||||||||||||||||||
     TP    78   1  1   13.734   13.782   .049       *-+++++++++++++++++++++++++++++++
 15  TN    79   1  1   13.768   13.782   .015       *-+++++++++++++++++++++++++++++++
     CPT   80   1  1   13.815   13.858   .044       -->  ||||||||||||||||||||||||||||||
     TN    81   1  1   13.840   13.858   .019       *-+++++++++++++++++++++++++++++++
     CPT   82   1  1   14.422   14.460   .039       -->  ||||||||||||||||||||||||||||||
     CPT   83   1  1   14.941   14.962   .022       -->  ||||||||||||||||||||||||||||||
 20  CPT   84   1  1   14.966   14.993   .028       -->  ||||||||||||||||||||||||||||||
     CPT   85   1  1   14.997   15.018   .022       -->  ||||||||||||||||||||||||||||||
     TP    86   1  1   15.795   15.816   .022       *-+++++++++++++++++++++++++++++++
     TP    87   1  1   15.996   16.020   .025       *-++*||||||||||||||||||||||||||||
     TP    88   1  1   16.874   16.898   .025       *-++-+++++++++++++++++++++++++++++
 25  CNT   89   1  1   20.136   20.151   .016       -->  ||  |||||||||||||||||||||||||||
     CNT   90   1  1   20.157   20.176   .020       -->  ||  |||||||||||||||||||||||||||
     GG    91   1  1   21.526   21.852   .327 Group0005  ||  |||||||||||||||||||||||||||
     CPT   92   1  1   22.257   22.304   .048       -->  ||  |||||||||||||||||||||||||||
     CNT   93   1  1   22.275   22.304   .030       -->  ||  |||||||||||||||||||||||||||
 30  CNT   94   1  1   22.307   22.322   .016       -->  ||  |||||||||||||||||||||||||||
     CPT   95   1  1   22.307   22.322   .016       -->  ||  |||||||||||||||||||||||||||
     CNT   96   1  1   22.324   22.338   .015       -->  ||  |||||||||||||||||||||||||||
     CNT   97   1  1   22.351   22.367   .017       -->  ||  |||||||||||||||||||||||||||
     CPT   98   8  1   22.351   22.367   .017       -->  ||  |||||||||||||||||||||||||||
 35  CNT   99   1  1   22.376   22.392   .017       -->  ||  |||||||||||||||||||||||||||
     CPT  100   8  1   22.376   22.392   .017       -->  ||  |||||||||||||||||||||||||||
     TN   101   1  1   23.300   23.324   .025       *-++*||||||||||||||||||||||||||||
     CPT  102   8  1   23.683   23.716   .034       -->  ||||||||||||||||||||||||||||||
     GG   103   1  1   24.001   27.969  3.969 Group0006  |||||||||||||||||||||||||||||||
 40  TN   104   1  1   24.119   24.431   .313       *-++++**||||||||||||||||||||||||
     CPT  105   1  1   24.283   24.352   .070     OS->  ||||  |||||||||||||||||||||||||
     TP   106   1  1   24.287   24.431   .145       *-++++--+*|||||||||||||||||||||||
     TN   107   1  1   24.433   24.514   .082       *-++++--*-*|||||||||||||||||||||
     TN   108   1  1   24.516   24.603   .088       *-++++-----*||||||||||||||||||||
 45  TN   109   8  1   24.605   24.703   .099       *-++++-------**|||||||||||||||||
     TN   110   1  1   24.743   24.854   .112       *-++++--------*|||||||||||||||||
     TP   111   1  1   24.863   25.001   .039       *-++++---------+*++*+*|||||||||
```

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The "Type" descriptor of the T1 (Id number 39) is "TP" showing that is T1 target is on the positive strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 111) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0004 (Id number 65) has the type descriptor "GG". The same is true for Group0006 (Id number 103).

Group0004 through Group0006 are described in table 2 as

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064C~A	-	1	negative	13.364	13.744	.381

Group0005

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064W	-	1	positive	21.526	21.852	.327

Group0006

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length

25

```
FLO9          -                     1 negative   24.001   27.969    3.969
      -------------------------------------------------------------------
```

   All of the data for the transient connectron 13 are pulled
together in the following table that is the "terse" description
of the connectron.

```
      -------------------------------------------------------------------
      Connectron Relationships - Global_Id  Type
                                      13  transient

      Control Sequences - Direction  Chromosome  C1/C2_Id      Start       Stop  Length
                          positive            1        36     12.572     12.788    .217

      Trigger Gene - Name      COG_Id      Start      Stop  Length
                 YAL064W-B  -            12.047    12.427    .381

      Target Sequences - Direction  Chromosome     T1_Id      Start       Stop  Length
                          positive            1        39     12.572     12.807    .236


                                             T2_Id      Start       Stop  Length
                                               111     24.863     25.001    .020


      Controlled Genes
      Local_Id  Chromosome  Group      Name        COG_Id    Direction     Start       Stop   Length
             1           1  Group0004 YAL064C-A  -           positive     13.364     13.744     .381
             2           1  Group0005 YAL064W    -           positive     21.526     21.852     .327
             3           1  Group0006 FLO9       -           positive     24.001     27.969    3.969

      Controlled Connectrons
      Local_Id  Chromosome  C1/C2_Id  Direction      Start       Stop   Length
             1           1        41  negative      12.964     12.908     .057
             2           1        42  positive      12.908     12.964     .057
             3           1        44  negative      12.986     12.966     .021
             4           1        45  positive      12.966     12.986     .021
             5           1        48  negative      13.099     13.028     .072
             6           1        50  positive      13.053     13.124     .072
             7           1        52  negative      13.246     13.105     .142
             8           1        53  positive      13.130     13.246     .117
             9           1        57  positive      13.253     13.290     .038
            10           1        60  negative      13.290     13.255     .036
            11           1        61  positive      13.295     13.315     .021
            12           1        63  negative      13.379     13.340     .040
            13           1        64  positive      13.341     13.380     .040
            14           1        66  positive      13.387     13.405     .019
            15           1        69  positive      13.566     13.582     .017
```

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16	1	71	positive	13.585	13.599	.016
17	1	75	positive	13.709	13.726	.018
18	1	77	positive	13.734	13.782	.049
19	1	80	positive	13.815	13.858	.044
20	1	82	positive	14.422	14.460	.039
21	1	83	positive	14.941	14.962	.022
22	1	84	positive	14.966	14.993	.028
23	1	85	positive	14.997	15.018	.022
24	1	89	negative	20.151	20.136	.016
25	1	90	negative	20.176	20.157	.020
26	1	92	positive	22.257	22.304	.048
27	1	93	negative	22.304	22.275	.030
28	1	94	negative	22.322	22.307	.016
29	1	95	positive	22.307	22.322	.016
30	1	96	negative	22.338	22.324	.015
31	1	97	negative	22.367	22.351	.017
32	1	98	positive	22.351	22.367	.017
33	1	99	negative	22.392	22.376	.017
34	1	100	positive	22.376	22.392	.017
35	1	102	positive	23.683	23.716	.034
36	1	105	positive	24.283	24.352	.070

The verbose description of the transient connectron 13 is:

In the Saccharomyces cerevisiae complete genome the transient
connectron number 13 is generated by the control sequence
(C1/C2) whose identifier number is 36. This control sequence is
on the positive strand of the genomic DNA of chromosome 1. The
genomic start and stop positions of this control sequence are
12.572 KB and 12.788 KB with a length of 0.217 KB. Expression of
the RNA for this connectron is triggered by the promotion of the
gene whose name is YAL064W-B. The genomic start and stop
positions of this gene are 12.047 KB and 12.427 KB and with a
length of 0.381 KB. This connectron causes stabilization of a
loop of DNA. The target sequences (T1-T2) are on the positive
strand of the genomic DNA on chromosome 1. The identifier number
of the initiating target sequence (T1) is 39. The genomic start

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and stop positions of this initiating target sequence are 12.572 KB and 12.807 KB with a length of 0.236 KB. The identifier number of the terminating target sequence (T2) is 111. The genomic start and stop positions of this terminating target sequence are 24.863 KB and 25.001 KB with a length of 0.020 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name YAL064C-A. The genomic start and stop positions of this gene are 13.364 KB and 13.744 KB with a length of 0.381 KB. (2) The gene that has the name YAL064W. The genomic start and stop positions of this gene are 21.526 KB and 21.852 KB with a length of 0.327 KB. (3) The gene that has the name FLO9. The genomic start and stop positions of this gene are 24.001 KB and 27.969 KB with a length of 3.969 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 41 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 12.964 KB and 12.908 KB with a length of 0.057 KB. (2) The connectron that has the identifier 42 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 12.908 KB and 12.964 KB with a length of 0.057 KB. (3) The connectron that has the identifier 44 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 12.986 KB and 12.966 KB with a length of 0.021 KB. (4) The connectron that has the identifier 45 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 12.966 KB and 12.986 KB with a length of 0.021 KB. (5) The connectron that has the identifier 48 is on chromosome 1 in the negative

direction. The genomic start and stop positions of this connectron are 13.099 KB and 13.028 KB with a length of 0.072 KB. (6) The connectron that has the identifier 50 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.053 KB and 13.124 KB with a length of 0.072 KB. (7) The connectron that has the identifier 52 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.246 KB and 13.105 KB with a length of 0.142 KB. (8) The connectron that has the identifier 53 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.130 KB and 13.246 KB with a length of 0.117 KB. (9) The connectron that has the identifier 57 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.253 KB and 13.290 KB with a length of 0.038 KB. (10) The connectron that has the identifier 60 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.290 KB and 13.255 KB with a length of 0.036 KB. (11) The connectron that has the identifier 61 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.295 KB and 13.315 KB with a length of 0.021 KB. (12) The connectron that has the identifier 63 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.379 KB and 13.340 KB with a length of 0.040 KB. (13) The connectron that has the identifier 64 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.341 KB and 13.380 KB with a length of 0.040 KB. (14) The connectron that has the identifier 66 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.387 KB and 13.405 KB with a length of 0.019

KB. (15) The connectron that has the identifier 69 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.566 KB and 13.582 KB with a length of 0.017 KB. (16) The connectron that has the

5   identifier 71 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.585 KB and 13.599 KB with a length of 0.016 KB. (17) The connectron that has the identifier 75 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

10 connectron are 13.709 KB and 13.726 KB with a length of 0.018 KB. (18) The connectron that has the identifier 77 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.734 KB and 13.782 KB with a length of 0.049 KB. (19) The connectron that has the

15 identifier 80 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.815 KB and 13.858 KB with a length of 0.044 KB. (20) The connectron that has the identifier 82 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

20 connectron are 14.422 KB and 14.460 KB with a length of 0.039 KB. (21) The connectron that has the identifier 83 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.941 KB and 14.962 KB with a length of 0.022 KB. (22) The connectron that has the

25 identifier 84 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.966 KB and 14.993 KB with a length of 0.028 KB. (23) The connectron that has the identifier 85 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

30 connectron are 14.997 KB and 15.018 KB with a length of 0.022 KB. (24) The connectron that has the identifier 89 is on chromosome 1 in the negative direction. The genomic start and

30

stop positions of this connectron are 20.151 KB and 20.136 KB with a length of 0.016 KB. (25) The connectron that has the identifier 90 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 20.176

5   KB and 20.157 KB with a length of 0.020 KB. (26) The connectron that has the identifier 92 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.257 KB and 22.304 KB with a length of 0.048 KB. (27) The connectron that has the identifier 93 is on

10 chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.304 KB and 22.275 KB with a length of 0.030 KB. (28) The connectron that has the identifier 94 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.322

15 KB and 22.307 KB with a length of 0.016 KB. (29) The connectron that has the identifier 95 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.307 KB and 22.322 KB with a length of 0.016 KB. (30) The connectron that has the identifier 96 is on

20 chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.338 KB and 22.324 KB with a length of 0.015 KB. (31) The connectron that has the identifier 97 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.367

25 KB and 22.351 KB with a length of 0.017 KB. (32) The connectron that has the identifier 98 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.351 KB and 22.367 KB with a length of 0.017 KB. (33) The connectron that has the identifier 99 is on

30 chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.392 KB and 22.376 KB with a length of 0.017 KB. (34) The connectron that has the

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identifier 100 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.376 KB and 22.392 KB with a length of 0.017 KB. (35) The connectron that has the identifier 102 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 23.683 KB and 23.716 KB with a length of 0.034 KB. (36) The connectron that has the identifier 105 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 24.283 KB and 24.352 KB with a length of 0.070 KB.

Addition of a Synthetic Connectron of Type 2 from Table 2

A synthetic connectron of type 2 in which the C1 and C2 are synthetic elements, the T1 is a synthetic element and the T2 is a natural element can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb and by modifying the DNA double-strand sequence at 705.150kb through 705.203kb for a length of 0.054kb.

Connectron 62521 is an example of a synthetic transient connectron. It is described as

| Global_Id | Chromosome | C1/C2 | | Chromosome | T1-T2 | | Connectron_Type |
		C1_Id	C2_Id		T1_Id	T2_Id	
62521	1	4651a	4651a	1	811a	975	transient

The C1/C2 source of the transient connectron 62521 is
represented in Table 1 as

```
     Type      Num Jobno  Chr   Start      Stop    Length GeneName
 5   CPT      4651a   1   1   4626.130  4626.166    .037            ||| ||  | |||| || |   ||
```

The "Type" descriptor of this transient C1/C2 connectron source
is "CPT". The letter "P" indicates that the C1/C2 connectron
source occurs on the positive strand of the double-stranded DNA
10 of the genome. The letter "N" in this place would indicate a
C1/C2 connectron source on the negative strand of the genomic
DNA. The letter "T" in this descriptor indicates a "transient"
connectron. Similarly, the letter "P" would indicate a
permanent connectron that is shown in a later example. The
15 "Start", "Stop" and "Length" descriptors throughout these
examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 62521 as shown in
Table 1 is represented as
20

```
     Type      Num Jobno  Chr   Start      Stop    Length GeneName
     TN        811a    1   1   705.150   705.203    .054            *-*
     TP        812     1   1   705.122   705.141    .020            *-+
     GG        813     1   1   705.316   706.980   1.665 Group0150   |
25   TN        814     1   1   707.013   707.028    .016            *-+
     TP        815     1   1   707.014   707.028    .015            *-+
     CPT       816     1   1   707.055   707.109    .055          -->  |
     TN        817     1   1   707.055   707.109    .055            *-+
     TP        818     1   1   707.055   707.109    .055            *-+
30   CPT       819     1   1   707.112   707.162    .051         OS->  |
     TN        820     1   1   707.112   707.162    .051            *-+
     TP        821     1   1   707.112   707.162    .051            *-+
     GG        822     1   1   707.557   710.688   3.131 Group0151   |
     CNT       823     1   1   710.633   710.647    .015         OS->  |
35   TN        824     1   1   710.633   710.647    .015            *-+
     CNT       825     1   1   710.652   710.666    .015          -->  |
     GG        826     1   1   710.828   712.755   1.927 Group0152   |
     TN        827     1   1   712.281   712.296    .016            *-+
     GG        828     1   1   712.781   714.421   1.641 Group0153   |
```

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TN	829	1	1	714.481	714.518	.038	*-+
CPT	830	1	1	714.481	714.519	.039	OS-> |
TP	831	1	1	714.482	714.519	.038	*-+
CPT	832	1	1	714.524	714.540	.017	--> |
TN	833	1	1	714.524	714.540	.017	*-+
TP	834	1	1	714.524	714.540	.017	*-+
CNT	835	1	1	714.543	714.593	.051	OS-> |
TN	836	1	1	714.543	714.593	.051	*-+
TP	837	1	1	714.543	714.593	.051	*-+
CPT	838	1	1	714.544	714.606	.063	OS-> |
GG	839	1	1	714.635	715.928	1.293 Group0154 |
GN	840	1	1	715.170	715.532	.363 ybfg |
TN	841	1	1	716.085	716.103	.019	*-+
TP	842	1	1	716.085	716.103	.019	*-+
GG	843	1	1	716.169	724.202	8.033 Group0155 |
CNT	844	1	1	720.278	720.296	.019	--> |
GN	845	1	1	720.279	724.202	3.924 kdpe |
TP	846	1	1	721.769	721.783	.015	*-+
TN	847	1	1	721.812	721.827	.016	*-+
GG	848	1	1	724.211	727.955	3.744 Group0156 |
TP	849	1	1	726.665	726.679	.015	*-+
GG	850	1	1	728.357	733.325	4.968 Group0157 |
GP	851	1	1	728.806	733.325	4.520 rhsc |
CPT	852	1	1	729.408	729.446	.039	--> |
TP	853	1	1	730.270	730.284	.015	*-+
CPT	854	1	1	730.443	730.457	.015	--> |
CPT	855	1	1	730.468	730.482	.015	--> |
CPT	856	1	1	730.484	730.507	.024	--> |
CPT	857	1	1	731.251	731.290	.040	--> |
TP	858	1	1	731.475	731.508	.034	*-+
TP	859	1	1	731.512	731.562	.051	*-+
TP	860	1	1	731.564	731.693	.130	*-+
TP	861	1	1	731.698	731.755	.058	*-+
TP	862	1	1	731.757	731.819	.063	*-+
TP	863	1	1	731.821	731.903	.083	*-+
TP	864	1	1	731.906	732.033	.128	*-+
CPT	865	1	1	731.994	732.016	.023	--> |
CPT	866	1	1	732.019	732.034	.016	--> |
TP	867	1	1	732.035	732.050	.016	*-+
TP	868	1	1	732.052	732.179	.128	*-+
CPT	869	1	1	732.065	732.179	.115	OS-> |
CPT	870	1	1	732.198	732.212	.015	--> |
TP	871	1	1	732.198	732.212	.015	*-|
CPT	872	1	1	732.214	732.233	.020	--> |
TP	873	1	1	732.214	732.233	.020	*-+
CPT	874	1	1	732.235	732.283	.049	--> |
TP	875	1	1	732.235	732.283	.049	*-+
CPT	876	1	1	732.306	732.326	.021	--> |

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```
      TP     877   1  1   732.306   732.326   .021              *-+
      CPT    878   1  1   732.328   732.452   .125          -->  |
      TP     879   1  1   732.328   732.482   .155              *-+
      CPT    880   1  1   732.454   732.482   .029          -->  |
  5   CPT    881   1  1   732.488   732.519   .032          -->  |
      TN     882   1  1   733.330   733.344   .015              *-+
      TP     883   1  1   733.330   733.344   .015              *-+
      TP     884   1  1   733.371   733.513   .143              *-+
      GG     885   1  1   733.443   735.442  2.000 Group0158    |
 10   TP     886   1  1   733.515   733.564   .050              *-+
      TP     887   1  1   733.569   733.626   .058              *-+
      TP     888   1  1   733.628   733.645   .018              *-+
      TP     889   1  1   733.647   733.696   .050              *-+
      TP     890   1  1   733.698   733.774   .077              *-+
 15   TP     891   1  1   733.776   733.904   .129              *-+
      CPT    892   1  1   733.865   733.887   .023         OS->  |
      CPT    893   1  1   733.890   733.905   .016          -->  |
      TP     894   1  1   733.906   734.050   .145              *-+
      CPT    895   1  1   733.936   734.050   .115          -->  |
 20   TP     896   1  1   734.052   734.075   .024              *-+
      CPT    897   1  1   734.052   734.139   .088          -->  |
      TP     898   1  1   734.084   734.139   .056              *-+
      TP     899   1  1   734.149   734.179   .031              *-+
      CPT    900   1  1   734.164   734.321   .158          -->  |
 25   TP     901   1  1   734.192   734.321   .130              *-+
      TP     902   1  1   734.323   734.378   .056              *-+
      CPT    903   1  1   734.323   734.381   .059          -->  |
      CPT    904   1  1   735.525   735.569   .045          -->  |
      TP     905   1  1   735.525   735.569   .045              *-+
 30   CPT    906   1  1   735.606   735.703   .098          -->  |
      TP     907   1  1   735.606   735.703   .098              *-+
      TP     908   1  1   735.707   735.721   .015              *-+
      CPT    909   1  1   735.707   735.728   .022          -->  |
      TP     910   1  1   735.749   735.803   .055              *-+
 35   CPT    911   1  1   735.807   735.964   .158         OS->  |
      TP     912   1  1   735.814   735.895   .082              *-+
      TP     913   1  1   735.905   735.934   .030              *-+
      TP     914   1  1   735.938   736.083   .146              *-+
      CPT    915   1  1   735.986   736.083   .098         OS->  |
 40   TP     916   1  1   736.152   736.173   .022              *-+
      TP     917   1  1   736.187   736.217   .031              *-+
      TP     918   1  1   736.219   736.265   .047              *-+
      TP     919   1  1   736.288   736.334   .047              *-+
      GG     920   1  1   736.327   737.184   .858 Group0159    |
 45   TP     921   1  1   736.349   736.469   .121              *-+
      TP     922   1  1   736.516   736.628   .113              *-+
      TP     923   1  1   736.630   736.645   .016              *-+
      TP     924   1  1   736.654   736.792   .139              *-+
```

	TN	925	1	1	736.654	736.809	.156	*-+
	TN	926	1	1	736.816	736.832	.017	*-+
	CPT	927	1	1	737.017	737.032	.016	--> |
	CPT	928	1	1	737.035	737.057	.023	--> |
5	TN	929	1	1	737.168	737.188	.021	*-++
	TP	930	1	1	737.196	737.290	.095	*-+
	CPT	931	1	1	737.261	737.275	.015	--> |
	CPT	932	1	1	737.278	737.292	.015	--> |
	TP	933	1	1	737.292	737.393	.102	*-+
10	GG	934	1	1	737.315	738.076	.762 Group0160	|
	TP	935	1	1	737.411	737.475	.065	*-+
	TP	936	1	1	737.479	737.557	.079	*-+
	TP	937	1	1	737.580	737.597	.018	*-+
	TP	938	1	1	737.605	737.626	.022	*-+
15	TP	939	1	1	737.633	737.648	.016	*-+
	TP	940	1	1	737.653	737.679	.027	*-+
	TP	941	1	1	737.683	737.752	.070	*-+
	TP	942	1	1	737.798	737.822	.025	*-+
	TP	943	1	1	737.828	737.895	.068	*-+
20	TP	944	1	1	737.897	737.931	.035	*-+
	CPT	945	1	1	737.930	737.967	.038	--> |
	TP	946	1	1	737.936	737.967	.032	*-+
	TP	947	1	1	737.970	737.988	.019	*-+
	TN	948	1	1	737.990	738.015	.026	*-+
25	TP	949	1	1	737.990	738.015	.026	*-+
	TN	950	1	1	738.019	738.051	.033	*-+
	TP	951	1	1	738.019	738.051	.033	*-++
	TP	952	1	1	738.053	738.074	.022	*-+
	TN	953	1	1	738.058	738.074	.017	*-+
30	TN	954	1	1	738.107	738.126	.020	*-+
	GG	955	1	1	738.224	740.148	1.925 Group0161	|
	TN	956	1	1	740.172	740.213	.042	*-+
	CNT	957	1	1	740.172	740.290	.119	OS-> |
	CPT	958	1	1	740.172	740.290	.119	OS-> |
35	TP	959	1	1	740.173	740.213	.041	*-+
	TP	960	1	1	740.216	740.241	.026	*-+
	TN	961	1	1	740.216	740.288	.073	*-+
	TP	962	1	1	740.244	740.288	.045	*-+
	GG	963	1	1	740.298	757.628	17.330 Group0162	|
40	GP	964	1	1	742.816	745.122	2.307 ybgj	|
	CPT	965	1	1	744.643	744.657	.015	--> |
	CPT	966	1	1	744.664	744.678	.015	--> |
	GP	967	1	1	754.400	756.896	2.497 sdhc	|
	CPT	968	1	1	755.680	755.714	.035	--> |
45	GP	969	1	1	756.912	757.628	.717 sdhb	|
	TN	970	1	1	757.626	757.712	.087	*-+
	CPT	971	1	1	757.628	757.712	.085	OS-> |
	TP	972	1	1	757.629	757.712	.084	*-+

36

```
GG       973    1 1   757.687   760.730    3.044 Group0163   |
CPT      974    1 1   757.717   757.736     .020       --> |
TN       975    1 1   757.718   757.753     .036       *-*
```

5   The "Type" descriptor of the T1 (Id number 811a) is "TN" showing
    that is T1 target is on the negative strand of the double-
    stranded genomic DNA. Because the T1 and the T2 targets have to
    be on the same strand, the T2 target (Id number 975) also has
    the type descriptor "TN".

10

    The T1-T2 loop diagram above can be read by tracing the path
    from the * of the T1 to the right to the appropriate *, then by
    tracing a path down the diagram to the first *, then by tracing
    a path left to the * of the T2. When horizontal lines

15 (indicated by -) intersect with other vertical lines (indicated
    by |) then the symbol at that point is changed to a +. When the
    T1-T2 loop does not contain an groups of genes then the vertical
    symbol (indicated by | or +) is changed to @ as shown below

20
```
Type      Num Jobno Chr   Start      Stop    Length GeneName
TN        xx    1 1   278.386   279.148     .763        *---*
XX        xx    1 1   278.387   278.416     .030        *    @
XX        xx    1 1   278.421   278.450     .030        *    @
TP        xx    1 1   278.452   278.892     .441        *---*
```
25

    Group0150 through Group0163 are described in Table 2 as

```
-----------------------------------------------------------------------
Group0150
```
30
```
Gene_Name  COG_Id        Chromosome  Direction    Start      Stop     Length
glns       COG0008   b            1  positive   705.316   706.980     1.665
-----------------------------------------------------------------------
Group0151
```
35
```
Gene_Name  COG_Id        Chromosome  Direction    Start      Stop     Length
ybfm       -         b            1  positive   707.557   708.963     1.407
ybfn       -         b            1  positive   709.013   709.339      .327
fur        COG0735   b            1  negative   709.423   709.869      .447
```

                                     37

```
flda        COG0716    b            1  negative   710.158   710.688      .531
        ---------------------------------------------------------------------
        Group0152

 5      Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        ybfe        -          b            1  negative   710.828   711.190      .363
        ybff       COG0596    b            1  negative   711.261   712.025      .765
        seqa       COG3057    b            1  positive   712.210   712.755      .546
        ---------------------------------------------------------------------
10      Group0153

        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        pgm        COG0033    b            1  positive   712.781   714.421     1.641
        ---------------------------------------------------------------------
15      Group0154

        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        ybfp        -          b            1  positive   714.635   715.129      .495
        ybfg        -          b            1  negative   715.170   715.532      .363
20      ybfh        -          b            1  negative   715.611   715.928      .318
        ---------------------------------------------------------------------
        Group0155

        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
25      pote       COG0531    b            1  negative   716.169   719.683     3.515
        kdpe       COG0745    b            1  negative   720.279   724.202     3.924
        ---------------------------------------------------------------------
        Group0156

30      Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        kdpb       COG2216    b            1  negative   724.211   726.259     2.049
        kdpa       COG2060    b            1  negative   726.282   727.955     1.674
        ---------------------------------------------------------------------
        Group0157
35
        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        ybfa        -          b            1  positive   728.357   728.563      .207
        rhsc        -          b            1  positive   728.806   733.325     4.520
        ---------------------------------------------------------------------
40      Group0158

        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        b0703      COG3209    b            1  positive   733.443   735.442     2.000
        ---------------------------------------------------------------------
45      Group0159

        Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
        ybfl        -          b            1  positive   736.327   737.184      .858
```

```
      -----------------------------------------------------------------------
      Group0160

      Gene_Name  COG_Id      Chromosome  Direction    Start     Stop    Length
5     ybfd       -           b                 1  positive   737.315  738.076    .762
      -----------------------------------------------------------------------
      Group0161

      Gene_Name  COG_Id      Chromosome  Direction    Start     Stop    Length
10    ybga       COG3272     b                 1  positive   738.224  740.148   1.925
      -----------------------------------------------------------------------
      Group0162

      Gene_Name  COG_Id      Chromosome  Direction    Start     Stop    Length
15    ybgh       COG3104     b                 1  negative   740.298  741.779   1.482
      ybgi       COG0327     b                 1  positive   742.050  742.793    .744
      ybgj       COG2049     b                 1  positive   742.816  745.122   2.307
      nei        COG0266     b                 1  positive   745.158  745.949    .792
      abrb       -           b                 1  negative   745.946  747.037   1.092
20    ybgo       -           b                 1  negative   747.144  748.930   1.787
      ybgq       -           b                 1  negative   748.945  751.401   2.457
      ybgd       -           b                 1  negative   751.452  752.018    .567
      glta       COG0372     b                 1  negative   752.408  753.691   1.284
      sdhc       COG2009     b                 1  positive   754.400  756.896   2.497
25    sdhb       COG0479     b                 1  positive   756.912  757.628    .717
      -----------------------------------------------------------------------
      Group0163

      Gene_Name  COG_Id      Chromosome  Direction    Start     Stop    Length
30    b0725      -           b                 1  positive   757.687  760.730   3.044
      -----------------------------------------------------------------------
```

All of the data for the transient connectron 62521 are pulled
together in the following table that is the "terse" description
35 of the connectron.

```
      -----------------------------------------------------------------------

      Connectron Relationships - Global_Id  Type
40                                   62521  transient

      Control Sequences - Direction  Chromosome  C1/C2_Id      Start      Stop   Length
                          positive            1      4651a  4626.130  4626.166     .036

45    Trigger Gene - Name      COG_Id       Start      Stop  Length
                      sms               4623.481  4626.116   2.636
```
39

	Target Sequences	- Direction	Chromosome	T1_Id	Start	Stop	Length
		negative	1	811a	705.150	705.203	.054

5

				T2_Id	Start	Stop	Length
				975	757.753	757.718	.036

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0150	glns	COG0008	positive	705.316	706.980	1.665
2	1	Group0151	ybfm	–	positive	707.557	710.688	3.131
3	1	Group0151	ybfn	–	positive	709.013	709.339	.327
4	1	Group0151	fur	COG0735	negative	709.869	709.423	.447
5	1	Group0151	flda	COG0716	negative	710.688	710.158	.531
6	1	Group0152	ybfe	–	positive	710.828	712.755	1.927
7	1	Group0152	ybff	COG0596	negative	712.025	711.261	.765
8	1	Group0152	seqa	COG3057	positive	712.210	712.755	.546
9	1	Group0153	pgm	COG0033	positive	712.781	714.421	1.641
10	1	Group0154	ybfp	–	positive	714.635	715.928	1.293
11	1	Group0154	ybfg	–	negative	715.532	715.170	.363
12	1	Group0154	ybfh	–	negative	715.928	715.611	.318
13	1	Group0155	pote	COG0531	positive	716.169	724.202	8.033
14	1	Group0155	kdpe	COG0745	negative	724.202	720.279	3.924
15	1	Group0156	kdpb	COG2216	positive	724.211	727.955	3.744
16	1	Group0156	kdpa	COG2060	negative	727.955	726.282	1.674
17	1	Group0157	ybfa	–	positive	728.357	733.325	4.968
18	1	Group0157	rhsc	–	positive	728.806	733.325	4.520
19	1	Group0158	b0703	COG3209	positive	733.443	735.442	2.000
20	1	Group0159	ybfl	–	positive	736.327	737.184	.858
21	1	Group0160	ybfd	–	positive	737.315	738.076	.762
22	1	Group0161	ybga	COG3272	positive	738.224	740.148	1.925
23	1	Group0162	ybgh	COG3104	positive	740.298	757.628	17.330
24	1	Group0162	ybgi	COG0327	positive	742.050	742.793	.744
25	1	Group0162	ybgj	COG2049	positive	742.816	745.122	2.307
26	1	Group0162	nei	COG0266	positive	745.158	745.949	.792
27	1	Group0162	abrb	–	negative	747.037	745.946	1.092
28	1	Group0162	ybgo	–	negative	748.930	747.144	1.787
29	1	Group0162	ybgq	–	negative	751.401	748.945	2.457
30	1	Group0162	ybgd	–	negative	752.018	751.452	.567
31	1	Group0162	glta	COG0372	negative	753.691	752.408	1.284
32	1	Group0162	sdhc	COG2009	positive	754.400	756.896	2.497
33	1	Group0162	sdhb	COG0479	positive	756.912	757.628	.717
34	1	Group0163	b0725	–	positive	757.687	760.730	3.044

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	816	positive	707.055	707.109	.055
2	1	819	positive	707.112	707.162	.051

3	1	823	negative	710.647	710.633	.015
4	1	825	negative	710.666	710.652	.015
5	1	830	positive	714.481	714.519	.039
6	1	832	positive	714.524	714.540	.017
7	1	835	negative	714.593	714.543	.051
8	1	838	positive	714.544	714.606	.063
9	1	844	negative	720.296	720.278	.019
10	1	852	positive	729.408	729.446	.039
11	1	854	positive	730.443	730.457	.015
12	1	855	positive	730.468	730.482	.015
13	1	856	positive	730.484	730.507	.024
14	1	857	positive	731.251	731.290	.040
15	1	865	positive	731.994	732.016	.023
16	1	866	positive	732.019	732.034	.016
17	1	869	positive	732.065	732.179	.115
18	1	870	positive	732.198	732.212	.015
19	1	872	positive	732.214	732.233	.020
20	1	874	positive	732.235	732.283	.049
21	1	876	positive	732.306	732.326	.021
22	1	878	positive	732.328	732.452	.125
23	1	880	positive	732.454	732.482	.029
24	1	881	positive	732.488	732.519	.032
25	1	892	positive	733.865	733.887	.023
26	1	893	positive	733.890	733.905	.016
27	1	895	positive	733.936	734.050	.115
28	1	897	positive	734.052	734.139	.088
29	1	900	positive	734.164	734.321	.158
30	1	903	positive	734.323	734.381	.059
31	1	904	positive	735.525	735.569	.045
32	1	906	positive	735.606	735.703	.098
33	1	909	positive	735.707	735.728	.022
34	1	911	positive	735.807	735.964	.158
35	1	915	positive	735.986	736.083	.098
36	1	927	positive	737.017	737.032	.016
37	1	928	positive	737.035	737.057	.023
38	1	931	positive	737.261	737.275	.015
39	1	932	positive	737.278	737.292	.015
40	1	945	positive	737.930	737.967	.038
41	1	957	negative	740.290	740.172	.119
42	1	958	positive	740.172	740.290	.119
43	1	965	positive	744.643	744.657	.015
44	1	966	positive	744.664	744.678	.015
45	1	968	positive	755.680	755.714	.035
46	1	971	positive	757.628	757.712	.085
47	1	974	positive	757.717	757.736	.020

The verbose description of the synthetic connectron 62521 is:

In the Escherichia coli K-12 MG1655 complete genome the transient connectron number 62521 is generated by the control sequence (C1/C2) whose identifier number is 4651a. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 4626.130 KB and 4626.166 KB with a length of 0.036 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is sms. The genomic start and stop positions of this gene are 4623.481 KB and 4626.116 KB and with a length of 2.636 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is 811a. The genomic start and stop positions of this initiating target sequence are 705.150 KB and 705.203 KB with a length of 0.054 KB. The identifier number of the terminating target sequence (T2) is 975. The genomic start and stop positions of this terminating target sequence are 757.753 KB and 757.718 KB with a length of 0.036 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name glns and with a COG identifier of COG0008. The genomic start and stop positions of this gene are 705.316 KB and 706.980 KB with a length of 1.665 KB. (2) The gene that has the name ybfm. The genomic start and stop positions of this gene are 707.557 KB and 710.688 KB with a length of 3.131 KB. (3) The gene that has the name ybfn. The genomic start and stop positions of this gene are 709.013 KB and 709.339 KB with a length of 0.327 KB. (4) The gene that has the name fur and with a COG identifier of COG0735.

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The genomic start and stop positions of this gene are 709.869 KB
and 709.423 KB with a length of 0.447 KB. (5) The gene that has
the name flda and with a COG identifier of COG0716. The genomic
start and stop positions of this gene are 710.688 KB and 710.158
KB with a length of 0.531 KB. (6) The gene that has the name
ybfe. The genomic start and stop positions of this gene are
710.828 KB and 712.755 KB with a length of 1.927 KB. (7) The
gene that has the name ybff and with a COG identifier of
COG0596. The genomic start and stop positions of this gene are
712.025 KB and 711.261 KB with a length of 0.765 KB. (8) The
gene that has the name seqa and with a COG identifier of
COG3057. The genomic start and stop positions of this gene are
712.210 KB and 712.755 KB with a length of 0.546 KB. (9) The
gene that has the name pgm and with a COG identifier of COG0033.
The genomic start and stop positions of this gene are 712.781 KB
and 714.421 KB with a length of 1.641 KB. (10) The gene that has
the name ybfp. The genomic start and stop positions of this
gene are 714.635 KB and 715.928 KB with a length of 1.293 KB.
(11) The gene that has the name ybfg. The genomic start and
stop positions of this gene are 715.532 KB and 715.170 KB with a
length of 0.363 KB. (12) The gene that has the name ybfh. The
genomic start and stop positions of this gene are 715.928 KB and
715.611 KB with a length of 0.318 KB. (13) The gene that has the
name pote and with a COG identifier of COG0531. The genomic
start and stop positions of this gene are 716.169 KB and 724.202
KB with a length of 8.033 KB. (14) The gene that has the name
kdpe and with a COG identifier of COG0745. The genomic start
and stop positions of this gene are 724.202 KB and 720.279 KB
with a length of 3.924 KB. (15) The gene that has the name kdpb
and with a COG identifier of COG2216. The genomic start and
stop positions of this gene are 724.211 KB and 727.955 KB with a
length of 3.744 KB. (16) The gene that has the name kdpa and

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with a COG identifier of COG2060. The genomic start and stop positions of this gene are 727.955 KB and 726.282 KB with a length of 1.674 KB. (17) The gene that has the name ybfa. The genomic start and stop positions of this gene are 728.357 KB and 733.325 KB with a length of 4.968 KB. (18) The gene that has the name rhsc. The genomic start and stop positions of this gene are 728.806 KB and 733.325 KB with a length of 4.520 KB. (19) The gene that has the name b0703 and with a COG identifier of COG3209. The genomic start and stop positions of this gene are 733.443 KB and 735.442 KB with a length of 2.000 KB. (20) The gene that has the name ybfl. The genomic start and stop positions of this gene are 736.327 KB and 737.184 KB with a length of 0.858 KB. (21) The gene that has the name ybfd. The genomic start and stop positions of this gene are 737.315 KB and 738.076 KB with a length of 0.762 KB. (22) The gene that has the name ybga and with a COG identifier of COG3272. The genomic start and stop positions of this gene are 738.224 KB and 740.148 KB with a length of 1.925 KB. (23) The gene that has the name ybgh and with a COG identifier of COG3104. The genomic start and stop positions of this gene are 740.298 KB and 757.628 KB with a length of 17.330 KB. (24) The gene that has the name ybgi and with a COG identifier of COG0327. The genomic start and stop positions of this gene are 742.050 KB and 742.793 KB with a length of 0.744 KB. (25) The gene that has the name ybgj and with a COG identifier of COG2049. The genomic start and stop positions of this gene are 742.816 KB and 745.122 KB with a length of 2.307 KB. (26) The gene that has the name nei and with a COG identifier of COG0266. The genomic start and stop positions of this gene are 745.158 KB and 745.949 KB with a length of 0.792 KB. (27) The gene that has the name abrb. The genomic start and stop positions of this gene are 747.037 KB and 745.946 KB with a length of 1.092 KB. (28) The gene that has the

name ybgo. The genomic start and stop positions of this gene are 748.930 KB and 747.144 KB with a length of 1.787 KB. (29) The gene that has the name ybgq. The genomic start and stop positions of this gene are 751.401 KB and 748.945 KB with a length of 2.457 KB. (30) The gene that has the name ybgd. The genomic start and stop positions of this gene are 752.018 KB and 751.452 KB with a length of 0.567 KB. (31) The gene that has the name glta and with a COG identifier of COG0372. The genomic start and stop positions of this gene are 753.691 KB and 752.408 KB with a length of 1.284 KB. (32) The gene that has the name sdhc and with a COG identifier of COG2009. The genomic start and stop positions of this gene are 754.400 KB and 756.896 KB with a length of 2.497 KB. (33) The gene that has the name sdhb and with a COG identifier of COG0479. The genomic start and stop positions of this gene are 756.912 KB and 757.628 KB with a length of 0.717 KB. (34) The gene that has the name b0725. The genomic start and stop positions of this gene are 757.687 KB and 760.730 KB with a length of 3.044 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 816 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.055 KB and 707.109 KB with a length of 0.055 KB. (2) The connectron that has the identifier 819 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.112 KB and 707.162 KB with a length of 0.051 KB. (3) The connectron that has the identifier 823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 710.647 KB and 710.633 KB with a length of 0.015 KB. (4) The connectron that has the identifier 825 is on chromosome 1 in the negative direction. The

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genomic start and stop positions of this connectron are 710.666 KB and 710.652 KB with a length of 0.015 KB. (5) The connectron that has the identifier 830 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

5   connectron are 714.481 KB and 714.519 KB with a length of 0.039 KB. (6) The connectron that has the identifier 832 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 714.524 KB and 714.540 KB with a length of 0.017 KB. (7) The connectron that has the

10   identifier 835 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 714.593 KB and 714.543 KB with a length of 0.051 KB. (8) The connectron that has the identifier 838 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

15   connectron are 714.544 KB and 714.606 KB with a length of 0.063 KB. (9) The connectron that has the identifier 844 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 720.296 KB and 720.278 KB with a length of 0.019 KB. (10) The connectron that has the

20   identifier 852 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 729.408 KB and 729.446 KB with a length of 0.039 KB. (11) The connectron that has the identifier 854 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

25   connectron are 730.443 KB and 730.457 KB with a length of 0.015 KB. (12) The connectron that has the identifier 855 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.468 KB and 730.482 KB with a length of 0.015 KB. (13) The connectron that has the

30   identifier 856 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.484 KB and 730.507 KB with a length of 0.024 KB. (14) The connectron

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that has the identifier 857 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.251 KB and 731.290 KB with a length of 0.040 KB. (15) The connectron that has the identifier 865 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.994 KB and 732.016 KB with a length of 0.023 KB. (16) The connectron that has the identifier 866 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.019 KB and 732.034 KB with a length of 0.016 KB. (17) The connectron that has the identifier 869 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.065 KB and 732.179 KB with a length of 0.115 KB. (18) The connectron that has the identifier 870 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.198 KB and 732.212 KB with a length of 0.015 KB. (19) The connectron that has the identifier 872 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.214 KB and 732.233 KB with a length of 0.020 KB. (20) The connectron that has the identifier 874 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.235 KB and 732.283 KB with a length of 0.049 KB. (21) The connectron that has the identifier 876 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.306 KB and 732.326 KB with a length of 0.021 KB. (22) The connectron that has the identifier 878 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.328 KB and 732.452 KB with a length of 0.125 KB. (23) The connectron that has the identifier 880 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

connectron are 732.454 KB and 732.482 KB with a length of 0.029
KB. (24) The connectron that has the identifier 881 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 732.488 KB and 732.519 KB
5   with a length of 0.032 KB. (25) The connectron that has the
identifier 892 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 733.865
KB and 733.887 KB with a length of 0.023 KB. (26) The connectron
that has the identifier 893 is on chromosome 1 in the positive
10   direction. The genomic start and stop positions of this
connectron are 733.890 KB and 733.905 KB with a length of 0.016
KB. (27) The connectron that has the identifier 895 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 733.936 KB and 734.050 KB
15   with a length of 0.115 KB. (28) The connectron that has the
identifier 897 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 734.052
KB and 734.139 KB with a length of 0.088 KB. (29) The connectron
that has the identifier 900 is on chromosome 1 in the positive
20   direction. The genomic start and stop positions of this
connectron are 734.164 KB and 734.321 KB with a length of 0.158
KB. (30) The connectron that has the identifier 903 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 734.323 KB and 734.381 KB
25   with a length of 0.059 KB. (31) The connectron that has the
identifier 904 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 735.525
KB and 735.569 KB with a length of 0.045 KB. (32) The connectron
that has the identifier 906 is on chromosome 1 in the positive
30   direction. The genomic start and stop positions of this
connectron are 735.606 KB and 735.703 KB with a length of 0.098
KB. (33) The connectron that has the identifier 909 is on

chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.707 KB and 735.728 KB with a length of 0.022 KB. (34) The connectron that has the identifier 911 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.807 KB and 735.964 KB with a length of 0.158 KB. (35) The connectron that has the identifier 915 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.986 KB and 736.083 KB with a length of 0.098 KB. (36) The connectron that has the identifier 927 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.017 KB and 737.032 KB with a length of 0.016 KB. (37) The connectron that has the identifier 928 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.035 KB and 737.057 KB with a length of 0.023 KB. (38) The connectron that has the identifier 931 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.261 KB and 737.275 KB with a length of 0.015 KB. (39) The connectron that has the identifier 932 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.278 KB and 737.292 KB with a length of 0.015 KB. (40) The connectron that has the identifier 945 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.930 KB and 737.967 KB with a length of 0.038 KB. (41) The connectron that has the identifier 957 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 740.290 KB and 740.172 KB with a length of 0.119 KB. (42) The connectron that has the identifier 958 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 740.172 KB and 740.290 KB

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with a length of 0.119 KB. (43) The connectron that has the identifier 965 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.643 KB and 744.657 KB with a length of 0.015 KB. (44) The connectron that has the identifier 966 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.664 KB and 744.678 KB with a length of 0.015 KB. (45) The connectron that has the identifier 968 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 755.680 KB and 755.714 KB with a length of 0.035 KB. (46) The connectron that has the identifier 971 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.628 KB and 757.712 KB with a length of 0.085 KB. (47) The connectron that has the identifier 974 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.717 KB and 757.736 KB with a length of 0.020 KB.

Addition of a Synthetic Connectron of Type 4 from Table 2

A synthetic connectron of type 4 in which the C1 and C2 are synthetic elements and the T1 and T2 are natural elements can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb.

Connectron 62520 is an example of a synthetic transient
connectron. It is described as

```
                          C1/C2                T1-T2
 5   Global_Id Chromosome  C1_Id  C2_Id Chromosome  T1_Id  T2_Id  Connectron_Type
        62520           1   4651a  4651a          1    809    975  transient
```

The C1/C2 source of the transient connectron 62520 is
represented in Table 1 as

10

```
     Type      Num Jobno  Chr   Start      Stop   Length GeneName
     CPT      4651a    1   1  4626.130  4626.166    .036           ||| || | |||| || | ' ||
```

The "Type" descriptor of this transient C1/C2 connectron source
15 is "CPT". The letter "P" indicates that the C1/C2 connectron
    source occurs on the positive strand of the double-stranded DNA
    of the genome. The letter "N" in this place would indicate a
    C1/C2 connectron source on the negative strand of the genomic
    DNA. The letter "T" in this descriptor indicates a "transient"
20 connectron. Similarly, the letter "P" would indicate a
    permanent connectron that is shown in a later example. The
    "Start", "Stop" and "Length" descriptors throughout these
    examples are given in kilo-bases (KB).

25 The T1-T2 target of the transient connectron 62520 as shown in
    Table 1 is represented as

```
        Type   Num Jobno  Chr   Start      Stop   Length GeneName
        TN     809    1   1   698.713   698.766    .054          *-+++*+++**++*+++++-+++++++++++
30      GG     810    1   1   698.797   705.113   6.316 Group0149  |||||||||||| ||||| ||||||||||||
        TN     811    1   1   705.121   705.141    .021          *-++*++++++++*+++++*+++++*+++++
        TP     812    1   1   705.122   705.141    .020          *-++-++++++++-++++++++++-+++++
        GG     813    1   1   705.316   706.980   1.665 Group0150  || ||||||||||| |||||||||||| |||||
        TN     814    1   1   707.013   707.028    .016          *-++*+++++++++*++++++++++*++++*
35      TP     815    1   1   707.014   707.028    .015          *-+++++++++++++++++++++++++++++-
        CPT    816    1   1   707.055   707.109    .055      -->  |||||||||||||||||||||||||||||||
        TN     817    1   1   707.055   707.109    .055          *-++++++++++*+*++++++++*+*+++++*
```

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```
   TP   818  1  1  707.055  707.109   .055              *-++++++++++-+-++++++++-+-++++++
   CPT  819  1  1  707.112  707.162   .051      OS->  ||||||||| | ||||||||| | ||||||
   TN   820  1  1  707.112  707.162   .051              *-++++*++++*+*+++++*+**++*++*++
   TP   821  1  1  707.112  707.162   .051              *-++++-++++++++++++-+-++++-+-++
 5 GG   822  1  1  707.557  710.688  3.131 Group0151   |||| ||||||||||||| | |||| | ||
   CNT  823  1  1  710.633  710.647   .015      OS->  |||| ||||||||||||| | |||| | ||
   TN   824  1  1  710.633  710.647   .015              *-++++-*||||||||||| | |||| | ||
   CNT  825  1  1  710.652  710.666   .015        -->  |||| ||||||||||||| | |||| | ||
   GG   826  1  1  710.828  712.755  1.927 Group0152   |||| ||||||||||||| | |||| | ||
10 TN   827  1  1  712.281  712.296   .016              *-++++--+++++++++++-+-++++-+-++
   GG   828  1  1  712.781  714.421  1.641 Group0153   |||| ||||||||||||| | |||| | ||
   TN   829  1  1  714.481  714.518   .038              *-++++**+++*++++++++*+-++++*+***
   CPT  830  1  1  714.481  714.519   .039      OS->  ||||||||| |||||||||||||||||
   TP   831  1  1  714.482  714.519   .038              *-++++++++++-++++++++++++++++--
15 CPT  832  1  1  714.524  714.540   .017        -->  ||||||||| |||||||||||||||||
   TN   833  1  1  714.524  714.540   .017              *-++++++++++*+*++++++++++++++**
   TP   834  1  1  714.524  714.540   .017              *-++++++++++-++++++++++++++++++
   CNT  835  1  1  714.543  714.593   .051      OS->  |||||||||| ||||||||||||||||||||
   TN   836  1  1  714.543  714.593   .051              *-++*++++++**+++++++*+++++++++
20 TP   837  1  1  714.543  714.593   .051              *-++-+++++++-+++++++++-++++++++
   CPT  838  1  1  714.544  714.606   .063      OS->  || ||||||||| |||||||||| ||||||||
   GG   839  1  1  714.635  715.928  1.293 Group0154   || ||||||||| |||||||||| ||||||||
   GN   840  1  1  715.170  715.532   .363 ybfg        || ||||||||| |||||||||| ||||||||
   TN   841  1  1  716.085  716.103   .019              *-++*+++++++*||||||||| ||||||||
25 TP   842  1  1  716.085  716.103   .019              *-+++++++++++++++++++*++++++++
   GG   843  1  1  716.169  724.202  8.033 Group0155   |||||||||||||||||||||||||||||||||
   CNT  844  1  1  720.278  720.296   .019        -->  |||||||||||||||||||||||||||||||||
   GN   845  1  1  720.279  724.202  3.924 kdpe        |||||||||||||||||||||||||||||||||
   TP   846  1  1  721.769  721.783   .015              *-++++++++++++++++++++++++++++
30 TN   847  1  1  721.812  721.827   .016              *-++++++++++++++++++++++++++++
   GG   848  1  1  724.211  727.955  3.744 Group0156   ||||||||||||||||||||||||||||||||
   TP   849  1  1  726.665  726.679   .015              *-++++++++++++++++++++++++++++
   GG   850  1  1  728.357  733.325  4.968 Group0157   |||||||||||||||||||||||||||||||||
   GP   851  1  1  728.806  733.325  4.520 rhsc        |||||||||||||||||||||||||||||||||
35 CPT  852  1  1  729.408  729.446   .039        -->  |||||||||||||||||||||||||||||||||
   TP   853  1  1  730.270  730.284   .015              *-++++++++++++++++++++++++++++
   CPT  854  1  1  730.443  730.457   .015        -->  |||||||||||||||||||||||||||||||||
   CPT  855  1  1  730.468  730.482   .015        -->  |||||||||||||||||||||||||||||||||
   CPT  856  1  1  730.484  730.507   .024        -->  |||||||||||||||||||||||||||||||||
40 CPT  857  1  1  731.251  731.290   .040        -->  |||||||||||||||||||||||||||||||||
   TP   858  1  1  731.475  731.508   .034              *-++++++++++++++++++++++++++++
   TP   859  1  1  731.512  731.562   .051              *-++++++++++++++++++++++++++++
   TP   860  1  1  731.564  731.693   .130              *-++++++++++++++++++++++++++++
   TP   861  1  1  731.698  731.755   .058              *-++++++++++++++++++++++++++++
45 TP   862  1  1  731.757  731.819   .063              *-++++++++++++++++++++++++++++
   TP   863  1  1  731.821  731.903   .083              *-++++++++++++++++++++++++++++
   TP   864  1  1  731.906  732.033   .128              *-++++++++++++++++++++++++++++
   CPT  865  1  1  731.994  732.016   .023        -->  |||||||||||||||||||||||||||||||||
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```
     CPT   866   1   1   732.019   732.034   .016            -->  ||||||||||||||||||||||||||||||||
     TP    867   1   1   732.035   732.050   .016            *-+++++++++++++++++++++++++++++++
     TP    868   1   1   732.052   732.179   .128            *-*++++++++++++++++++++++++++++++
     CPT   869   1   1   732.065   732.179   .115       OS-> ||||||||||||||||||||||||||||||||
  5  CPT   870   1   1   732.198   732.212   .015            -->  ||||||||||||||||||||||||||||||||
     TP    871   1   1   732.198   732.212   .015            *-*||||||||||||||||||||||||||||||
     CPT   872   1   1   732.214   732.233   .020            -->  ||||||||||||||||||||||||||||||||
     TP    873   1   1   732.214   732.233   .020            *-+++++++++++++++++++++++++++++++
     CPT   874   1   1   732.235   732.283   .049            -->  ||||||||||||||||||||||||||||||||
 10  TP    875   1   1   732.235   732.283   .049            *-+++++++++++++++++++++++++++++++
     CPT   876   1   1   732.306   732.326   .021            -->  ||||||||||||||||||||||||||||||||
     TP    877   1   1   732.306   732.326   .021            *-+++++++++++++++++++++++++++++++
     CPT   878   1   1   732.328   732.452   .125            -->  ||||||||||||||||||||||||||||||||
     TP    879   1   1   732.328   732.482   .155            *-+++++++++++++++++++++++++++++++
 15  CPT   880   1   1   732.454   732.482   .029            -->  ||||||||||||||||||||||||||||||||
     CPT   881   1   1   732.488   732.519   .032            -->  ||||||||||||||||||||||||||||||||
     TN    882   1   1   733.330   733.344   .015            *-+++++++++++++++++++++++++++++++
     TP    883   1   1   733.330   733.344   .015            *-+++++++++++++++++++++++++++++++
     TP    884   1   1   733.371   733.513   .143            *-+++++++++++++++++++++++++++++++
 20  GG    885   1   1   733.443   735.442  2.000 Group0158  ||||||||||||||||||||||||||||||||
     TP    886   1   1   733.515   733.564   .050            *-+++++++++++++++++++++++++++++++
     TP    887   1   1   733.569   733.626   .058            *-+++++++++++++++++++++++++++++++
     TP    888   1   1   733.628   733.645   .018            *-+++++++++++++++++++++++++++++++
     TP    889   1   1   733.647   733.696   .050            *-+++++++++++++++++++++++++++++++
 25  TP    890   1   1   733.698   733.774   .077            *-+++++++++++++++++++++++++++++++
     TP    891   1   1   733.776   733.904   .129            *-+++++++++++++++++++++++++++++++
     CPT   892   1   1   733.865   733.887   .023       OS-> ||||||||||||||||||||||||||||||||
     CPT   893   1   1   733.890   733.905   .016            -->  ||||||||||||||||||||||||||||||||
     TP    894   1   1   733.906   734.050   .145            *-+*+++++++++++++++++++++++++++++
 30  CPT   895   1   1   733.936   734.050   .115            -->  | ||||||||||||||||||||||||||||||
     TP    896   1   1   734.052   734.075   .024            *-+-+++++++++++++++++++++++++++++
     CPT   897   1   1   734.052   734.139   .088            -->  | ||||||||||||||||||||||||||||||
     TP    898   1   1   734.084   734.139   .056            *-*-+++++++++++++++++++++++++++++
     TP    899   1   1   734.149   734.179   .031            *---+++++++++++++++++++++++++++++
 35  CPT   900   1   1   734.164   734.321   .158            -->  ||||||||||||||||||||||||||||||||
     TP    901   1   1   734.192   734.321   .130            *---+++++++++++++++++++++++++++++
     TP    902   1   1   734.323   734.378   .056            *---+++++++++++++++++++++++++++++
     CPT   903   1   1   734.323   734.381   .059            -->  ||||||||||||||||||||||||||||||||
     CPT   904   1   1   735.525   735.569   .045            -->  ||||||||||||||||||||||||||||||||
 40  TP    905   1   1   735.525   735.569   .045            *-* ||||||||||||||||||||||||||||||
     CPT   906   1   1   735.606   735.703   .098            -->  | ||||||||||||||||||||||||||||||
     TP    907   1   1   735.606   735.703   .098            *-+*+++++++++++++++++++++++++++++
     TP    908   1   1   735.707   735.721   .015            *-+++++++++++++++++++++++++++++++
     CPT   909   1   1   735.707   735.728   .022            -->  ||||||||||||||||||||||||||||||||
 45  TP    910   1   1   735.749   735.803   .055            *-+++++++++++++++++++++++++++++++
     CPT   911   1   1   735.807   735.964   .158       OS-> ||||||||||||||||||||||||||||||||
     TP    912   1   1   735.814   735.895   .082            *-+++++++++++++++++++++++++++++++
     TP    913   1   1   735.905   735.934   .030            *-+++++++++++++++++++++++++++++++
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	TP	914	1	1	735.938	736.083	.146	*-+++++++++++++++++++++++++++++
	CPT	915	1	1	735.986	736.083	.098	OS-> |||||||||||||||||||||||||||||||
	TP	916	1	1	736.152	736.173	.022	*-+++++++++++++++++++++++++++++
	TP	917	1	1	736.187	736.217	.031	*-+++++++++++++++++++++++++++++
5	TP	918	1	1	736.219	736.265	.047	*-+++++++++++++++++++++++++++++
	TP	919	1	1	736.288	736.334	.047	*-+++++++++++++++++++++++++++++
	GG	920	1	1	736.327	737.184	.858	Group0159 |||||||||||||||||||||||||||||||
	TP	921	1	1	736.349	736.469	.121	*-+++++++++++++++++++++++++++++
	TP	922	1	1	736.516	736.628	.113	*-+++++++++++++++++++++++++++++
10	TP	923	1	1	736.630	736.645	.016	*-+++++++++++++++++++++++++++++
	TP	924	1	1	736.654	736.792	.139	*-+++++++++++++++++++++++++++++
	TN	925	1	1	736.654	736.809	.156	*-+++++++++++++++++++++++++++++
	TN	926	1	1	736.816	736.832	.017	*-+++++++++++++++++++++++++++++
	CPT	927	1	1	737.017	737.032	.016	--> |||||||||||||||||||||||||||||||
15	CPT	928	1	1	737.035	737.057	.023	--> |||||||||||||||||||||||||||||||
	TN	929	1	1	737.168	737.188	.021	*-+++++++++++++++++++++++++++++
	TP	930	1	1	737.196	737.290	.095	*-**+++++++++++++++++++++++++++
	CPT	931	1	1	737.261	737.275	.015	--> |||||||||||||||||||||||||||||||
	CPT	932	1	1	737.278	737.292	.015	--> |||||||||||||||||||||||||||||||
20	TP	933	1	1	737.292	737.393	.102	*---+++++++++++++++++++++++++++
	GG	934	1	1	737.315	738.076	.762	Group0160 |||||||||||||||||||||||||||||||
	TP	935	1	1	737.411	737.475	.065	*---+++++++++++++++++++++++++++
	TP	936	1	1	737.479	737.557	.079	*---+++++++++++++++++++++++++++
	TP	937	1	1	737.580	737.597	.018	*---+++++++++++++++++++++++++++
25	TP	938	1	1	737.605	737.626	.022	*---+++++++++++++++++++++++++++
	TP	939	1	1	737.633	737.648	.016	*---+++++++++++++++++++++++++++
	TP	940	1	1	737.653	737.679	.027	*---+++++++++++++++++++++++++++
	TP	941	1	1	737.683	737.752	.070	*---+++++++++++++++++++++++++++
	TP	942	1	1	737.798	737.822	.025	*---+++++++++++++++++++++++++++
30	TP	943	1	1	737.828	737.895	.068	*---+++++++++++++++++++++++++++
	TP	944	1	1	737.897	737.931	.035	*---+++++++++++++++++++++++++++
	CPT	945	1	1	737.930	737.967	.038	--> |||||||||||||||||||||||||||||||
	TP	946	1	1	737.936	737.967	.032	*---+++++++++++++++++++++++++++
	TP	947	1	1	737.970	737.988	.019	*---+++++++++++++++++++++++++++
35	TN	948	1	1	737.990	738.015	.026	*---+++++++++++++++++++++++++++
	TP	949	1	1	737.990	738.015	.026	*---+++++++++++++++++++++++++++
	TN	950	1	1	738.019	738.051	.033	*---+++++++++++++++++++++++++++
	TP	951	1	1	738.019	738.051	.033	*---+++++++++++++++++++++++++++
	TP	952	1	1	738.053	738.074	.022	*---+++++++++++++++++++++++++++
40	TN	953	1	1	738.058	738.074	.017	*---+++++++++++++++++++++++++++
	TN	954	1	1	738.107	738.126	.020	*---+++++++++++++++++++++++++++
	GG	955	1	1	738.224	740.148	1.925	Group0161 |||||||||||||||||||||||||||||||
	TN	956	1	1	740.172	740.213	.042	*-**+++*++++*+++*+++++++*+++++
	CNT	957	1	1	740.172	740.290	.119	OS-> |||||| |||| ||| ||||||| |||||||
45	CPT	958	1	1	740.172	740.290	.119	OS-> |||||| |||| ||| ||||||| |||||||
	TP	959	1	1	740.173	740.213	.041	*-+++++++*++++*+++**+++++*+++++
	TP	960	1	1	740.216	740.241	.026	*-++++++++++++++++-++++++++++++
	TN	961	1	1	740.216	740.288	.073	*-+++*+++++++++**++-++++++++++++

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```
      TP       962    1  1   740.244   740.288    .045            *-++!-++++++++--++*+++**+++++++
      GG       963    1  1   740.298   757.628  17.330 Group0162   ||| ||||||||| ||||||  |||||||
      GP       964    1  1   742.816   745.122   2.307 ybgj        ||| ||||||||| ||||||  |||||||
      CPT      965    1  1   744.643   744.657    .015        -->  ||| ||||||||| ||||||  |||||||
      CPT      966    1  1   744.664   744.678    .015        -->  ||| ||||||||| ||||||  |||||||
      GP       967    1  1   754.400   756.896   2.497 sdhc        ||| ||||||||| ||||||  |||||||
      CPT      968    1  1   755.680   755.714    .035        -->  ||| ||||||||| ||||||  |||||||
      GP       969    1  1   756.912   757.628    .717 sdhb        ||| ||||||||| ||||||  |||||||
      TN       970    1  1   757.626   757.712    .087            *-*+**+++*++++**++++++**+++*+++
      CPT      971    1  1   757.628   757.712    .085        OS->  | ||||| ||||||| ||||||||||| |||
      TP       972    1  1   757.629   757.712    .084            *--+-+++*-++++++-+*+++++++++-+++
      GG       973    1  1   757.687   760.730   3.044 Group0163    | |||  |||||||| | ||||||||| |||
      CPT      974    1  1   757.717   757.736    .020        -->   | |||  |||||||| | ||||||||| |||
      TN       975    1  1   757.718   757.753    .036            *-*+*+++*****+++++*+-+*+++++++-+++
```

The "Type" descriptor of the T1 (Id number 809) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 975) also has the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

```
      Type    Num Jobno  Chr   Start     Stop    Length  GeneName
      TN       xx    1  1    278.386   279.148    .763             *---*
      XX       xx    1  1    278.387   278.416    .030             *   @
      XX       xx    1  1    278.421   278.450    .030             *   @
      TP       xx    1  1    278.452   278.892    .441             *---*
```

Group0149 through Group0163 are described in Table 2 as

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Group0149

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
nagd	COG0647	b	1	negative	698.797	699.549	.753
nagc	COG1940	b	1	negative	699.597	700.817	1.221
naga	COG1820	b	1	negative	700.826	701.974	1.149
nagb	COG0363	b	1	negative	702.034	702.834	.801
nage	COG1264	b	1	positive	703.167	705.113	1.947

Group0150

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
glns	COG0008	b	1	positive	705.316	706.980	1.665

Group0151

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfm	-	b	1	positive	707.557	708.963	1.407
ybfn	-	b	1	positive	709.013	709.339	.327
fur	COG0735	b	1	negative	709.423	709.869	.447
flda	COG0716	b	1	negative	710.158	710.688	.531

Group0152

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfe	-	b	1	negative	710.828	711.190	.363
ybff	COG0596	b	1	negative	711.261	712.025	.765
seqa	COG3057	b	1	positive	712.210	712.755	.546

Group0153

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
pgm	COG0033	b	1	positive	712.781	714.421	1.641

Group0154

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfp	-	b	1	positive	714.635	715.129	.495
ybfg	-	b	1	negative	715.170	715.532	.363
ybfh	-	b	1	negative	715.611	715.928	.318

Group0155

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
pote	COG0531	b	1	negative	716.169	719.683	3.515
kdpe	COG0745	b	1	negative	720.279	724.202	3.924

Group0156

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
kdpb	COG2216	b	1	negative	724.211	726.259	2.049
kdpa	COG2060	b	1	negative	726.282	727.955	1.674

Group0157

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfa	-	b	1	positive	728.357	728.563	.207
rhsc	-	b	1	positive	728.806	733.325	4.520

Group0158

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
b0703	COG3209	b	1	positive	733.443	735.442	2.000

Group0159

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfl	-	b	1	positive	736.327	737.184	.858

Group0160

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybfd	-	b	1	positive	737.315	738.076	.762

Group0161

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybga	COG3272	b	1	positive	738.224	740.148	1.925

Group0162

Gene_Name	COG_Id	Chromosome		Direction	Start	Stop	Length
ybgh	COG3104	b	1	negative	740.298	741.779	1.482
ybgi	COG0327	b	1	positive	742.050	742.793	.744
ybgj	COG2049	b	1	positive	742.816	745.122	2.307
nei	COG0266	b	1	positive	745.158	745.949	.792
abrb	-	b	1	negative	745.946	747.037	1.092
ybgo	-	b	1	negative	747.144	748.930	1.787
ybgq	-	b	1	negative	748.945	751.401	2.457
ybgd	-	b	1	negative	751.452	752.018	.567
glta	COG0372	b	1	negative	752.408	753.691	1.284
sdhc	COG2009	b	1	positive	754.400	756.896	2.497
sdhb	COG0479	b	1	positive	756.912	757.628	.717

Group0163

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```
Gene_Name  COG_Id        Chromosome  Direction   Start      Stop      Length
b0725      -          b        1  positive  757.687   760.730    3.044
------------------------------------------------------------------
```

All of the data for the transient connectron 62520 are pulled
together in the following table that is the "terse" description
of the connectron.

```
------------------------------------------------------------------

Connectron Relationships - Global_Id  Type
                            62520  transient


Control Sequences - Direction  Chromosome  C1/C2_Id     Start      Stop   Length
                    positive       1       4651a    4626.130  4626.166    .036


Trigger Gene - Name      COG_Id      Start      Stop   Length
               sms              4623.481  4626.116   2.636


Target Sequences  - Direction  Chromosome    T1_Id     Start      Stop   Length
                    negative       1        809    698.766   698.713    .054


                                             T2_Id     Start      Stop   Length
                                             975    757.753   757.718    .036


Controlled Genes
Local_Id  Chromosome  Group     Name     COG_Id   Direction    Start     Stop    Length
       1         1  Group0149 nagd   COG0647  positive   698.797  705.113   6.316
       2         1  Group0149 nagc   COG1940  negative   700.817  699.597   1.221
       3         1  Group0149 naga   COG1820  negative   701.974  700.826   1.149
       4         1  Group0149 nagb   COG0363  negative   702.834  702.034    .801
       5         1  Group0149 nage   COG1264  positive   703.167  705.113   1.947
       6         1  Group0150 glns   COG0008  positive   705.316  706.980   1.665
       7         1  Group0151 ybfm   -        positive   707.557  710.688   3.131
       8         1  Group0151 ybfn   -        positive   709.013  709.339    .327
       9         1  Group0151 fur    COG0735  negative   709.869  709.423    .447
      10         1  Group0151 flda   COG0716  negative   710.688  710.158    .531
      11         1  Group0152 ybfe   -        positive   710.828  712.755   1.927
      12         1  Group0152 ybff   COG0596  negative   712.025  711.261    .765
      13         1  Group0152 seqa   COG3057  positive   712.210  712.755    .546
      14         1  Group0153 pgm    COG0033  positive   712.781  714.421   1.641
      15         1  Group0154 ybfp   -        positive   714.635  715.928   1.293
      16         1  Group0154 ybfg   -        negative   715.532  715.170    .363
      17         1  Group0154 ybfh   -        negative   715.928  715.611    .318
      18         1  Group0155 pote   COG0531  positive   716.169  724.202   8.033
      19         1  Group0155 kdpe   COG0745  negative   724.202  720.279   3.924
```

20	1	Group0156 kdpb	COG2216	positive	724.211	727.955	3.744
21	1	Group0156 kdpa	COG2060	negative	727.955	726.282	1.674
22	1	Group0157 ybfa	–	positive	728.357	733.325	4.968
23	1	Group0157 rhsc	–	positive	728.806	733.325	4.520
24	1	Group0158 b0703	COG3209	positive	733.443	735.442	2.000
25	1	Group0159 ybfl	–	positive	736.327	737.184	.858
26	1	Group0160 ybfd	–	positive	737.315	738.076	.762
27	1	Group0161 ybga	COG3272	positive	738.224	740.148	1.925
28	1	Group0162 ybgh	COG3104	positive	740.298	757.628	17.330
29	1	Group0162 ybgi	COG0327	positive	742.050	742.793	.744
30	1	Group0162 ybgj	COG2049	positive	742.816	745.122	2.307
31	1	Group0162 nei	COG0266	positive	745.158	745.949	.792
32	1	Group0162 abrb	–	negative	747.037	745.946	1.092
33	1	Group0162 ybgo	–	negative	748.930	747.144	1.787
34	1	Group0162 ybgq	–	negative	751.401	748.945	2.457
35	1	Group0162 ybgd	–	negative	752.018	751.452	.567
36	1	Group0162 glta	COG0372	negative	753.691	752.408	1.284
37	1	Group0162 sdhc	COG2009	positive	754.400	756.896	2.497
38	1	Group0162 sdhb	COG0479	positive	756.912	757.628	.717
39	1	Group0163 b0725	–	positive	757.687	760.730	3.044

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	816	positive	707.055	707.109	.055
2	1	819	positive	707.112	707.162	.051
3	1	823	negative	710.647	710.633	.015
4	1	825	negative	710.666	710.652	.015
5	1	830	positive	714.481	714.519	.039
6	1	832	positive	714.524	714.540	.017
7	1	835	negative	714.593	714.543	.051
8	1	838	positive	714.544	714.606	.063
9	1	844	negative	720.296	720.278	.019
10	1	852	positive	729.408	729.446	.039
11	1	854	positive	730.443	730.457	.015
12	1	855	positive	730.468	730.482	.015
13	1	856	positive	730.484	730.507	.024
14	1	857	positive	731.251	731.290	.040
15	1	865	positive	731.994	732.016	.023
16	1	866	positive	732.019	732.034	.016
17	1	869	positive	732.065	732.179	.115
18	1	870	positive	732.198	732.212	.015
19	1	872	positive	732.214	732.233	.020
20	1	874	positive	732.235	732.283	.049
21	1	876	positive	732.306	732.326	.021
22	1	878	positive	732.328	732.452	.125
23	1	880	positive	732.454	732.482	.029
24	1	881	positive	732.488	732.519	.032
25	1	892	positive	733.865	733.887	.023

```
        26        1        893    positive   733.890    733.905    .016
        27        1        895    positive   733.936    734.050    .115
        28        1        897    positive   734.052    734.139    .088
        29        1        900    positive   734.164    734.321    .158
   5    30        1        903    positive   734.323    734.381    .059
        31        1        904    positive   735.525    735.569    .045
        32        1        906    positive   735.606    735.703    .098
        33        1        909    positive   735.707    735.728    .022
        34        1        911    positive   735.807    735.964    .158
  10    35        1        915    positive   735.986    736.083    .098
        36        1        927    positive   737.017    737.032    .016
        37        1        928    positive   737.035    737.057    .023
        38        1        931    positive   737.261    737.275    .015
        39        1        932    positive   737.278    737.292    .015
  15    40        1        945    positive   737.930    737.967    .038
        41        1        957    negative   740.290    740.172    .119
        42        1        958    positive   740.172    740.290    .119
        43        1        965    positive   744.643    744.657    .015
        44        1        966    positive   744.664    744.678    .015
  20    45        1        968    positive   755.680    755.714    .035
        46        1        971    positive   757.628    757.712    .085
        47        1        974    positive   757.717    757.736    .020


        ------------------------------------------------------------------

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The verbose description of the synthetic connectron 62520 is:

In the Escherichia coli K-12 MG1655 complete genome the
transient connectron number 62520 is generated by the control
  30   sequence (C1/C2) whose identifier number is 4651a. This control
sequence is on the positive strand of the genomic DNA of
chromosome 1. The genomic start and stop positions of this
control sequence are 4626.130 KB and 4626.166 KB with a length
of 0.036 KB. Expression of the RNA for this connectron is
  35   triggered by the promotion of the gene whose name is sms. The
genomic start and stop positions of this gene are 4623.481 KB
and 4626.116 KB and with a length of 2.636 KB. This connectron
causes stabilization of a loop of DNA.  The target sequences
(T1-T2) are on the negative strand of the genomic DNA on
  40   chromosome 1. The identifier number of the initiating target
```

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sequence (T1) is 809. The genomic start and stop positions of this initiating target sequence are 698.766 KB and 698.713 KB with a length of 0.054 KB. The identifier number of the terminating target sequence (T2) is 975. The genomic start and stop positions of this terminating target sequence are 757.753 KB and 757.718 KB with a length of 0.036 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name nagd and with a COG identifier of COG0647. The genomic start and stop positions of this gene are 698.797 KB and 705.113 KB with a length of 6.316 KB. (2) The gene that has the name nagc and with a COG identifier of COG1940. The genomic start and stop positions of this gene are 700.817 KB and 699.597 KB with a length of 1.221 KB. (3) The gene that has the name naga and with a COG identifier of COG1820. The genomic start and stop positions of this gene are 701.974 KB and 700.826 KB with a length of 1.149 KB. (4) The gene that has the name nagb and with a COG identifier of COG0363. The genomic start and stop positions of this gene are 702.834 KB and 702.034 KB with a length of 0.801 KB. (5) The gene that has the name nage and with a COG identifier of COG1264. The genomic start and stop positions of this gene are 703.167 KB and 705.113 KB with a length of 1.947 KB. (6) The gene that has the name glns and with a COG identifier of COG0008. The genomic start and stop positions of this gene are 705.316 KB and 706.980 KB with a length of 1.665 KB. (7) The gene that has the name ybfm. The genomic start and stop positions of this gene are 707.557 KB and 710.688 KB with a length of 3.131 KB. (8) The gene that has the name ybfn. The genomic start and stop positions of this gene are 709.013 KB and 709.339 KB with a length of 0.327 KB. (9) The gene that has the name fur and with a COG identifier of COG0735.

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The genomic start and stop positions of this gene are 709.869 KB and 709.423 KB with a length of 0.447 KB. (10) The gene that has the name flda and with a COG identifier of COG0716. The genomic start and stop positions of this gene are 710.688 KB and 710.158 KB with a length of 0.531 KB. (11) The gene that has the name ybfe. The genomic start and stop positions of this gene are 710.828 KB and 712.755 KB with a length of 1.927 KB. (12) The gene that has the name ybff and with a COG identifier of COG0596. The genomic start and stop positions of this gene are 712.025 KB and 711.261 KB with a length of 0.765 KB. (13) The gene that has the name seqa and with a COG identifier of COG3057. The genomic start and stop positions of this gene are 712.210 KB and 712.755 KB with a length of 0.546 KB. (14) The gene that has the name pgm and with a COG identifier of COG0033. The genomic start and stop positions of this gene are 712.781 KB and 714.421 KB with a length of 1.641 KB. (15) The gene that has the name ybfp. The genomic start and stop positions of this gene are 714.635 KB and 715.928 KB with a length of 1.293 KB. (16) The gene that has the name ybfg. The genomic start and stop positions of this gene are 715.532 KB and 715.170 KB with a length of 0.363 KB. (17) The gene that has the name ybfh. The genomic start and stop positions of this gene are 715.928 KB and 715.611 KB with a length of 0.318 KB. (18) The gene that has the name pote and with a COG identifier of COG0531. The genomic start and stop positions of this gene are 716.169 KB and 724.202 KB with a length of 8.033 KB. (19) The gene that has the name kdpe and with a COG identifier of COG0745. The genomic start and stop positions of this gene are 724.202 KB and 720.279 KB with a length of 3.924 KB. (20) The gene that has the name kdpb and with a COG identifier of COG2216. The genomic start and stop positions of this gene are 724.211 KB and 727.955 KB with a length of 3.744 KB. (21) The gene that has the name kdpa and

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with a COG identifier of COG2060. The genomic start and stop
positions of this gene are 727.955 KB and 726.282 KB with a
length of 1.674 KB. (22) The gene that has the name ybfa. The
genomic start and stop positions of this gene are 728.357 KB and
733.325 KB with a length of 4.968 KB. (23) The gene that has the
name rhsc. The genomic start and stop positions of this gene
are 728.806 KB and 733.325 KB with a length of 4.520 KB. (24)
The gene that has the name b0703 and with a COG identifier of
COG3209. The genomic start and stop positions of this gene are
733.443 KB and 735.442 KB with a length of 2.000 KB. (25) The
gene that has the name ybfl. The genomic start and stop
positions of this gene are 736.327 KB and 737.184 KB with a
length of 0.858 KB. (26) The gene that has the name ybfd. The
genomic start and stop positions of this gene are 737.315 KB and
738.076 KB with a length of 0.762 KB. (27) The gene that has the
name ybga and with a COG identifier of COG3272. The genomic
start and stop positions of this gene are 738.224 KB and 740.148
KB with a length of 1.925 KB. (28) The gene that has the name
ybgh and with a COG identifier of COG3104. The genomic start
and stop positions of this gene are 740.298 KB and 757.628 KB
with a length of 17.330 KB. (29) The gene that has the name ybgi
and with a COG identifier of COG0327. The genomic start and
stop positions of this gene are 742.050 KB and 742.793 KB with a
length of 0.744 KB. (30) The gene that has the name ybgj and
with a COG identifier of COG2049. The genomic start and stop
positions of this gene are 742.816 KB and 745.122 KB with a
length of 2.307 KB. (31) The gene that has the name nei and with
a COG identifier of COG0266. The genomic start and stop
positions of this gene are 745.158 KB and 745.949 KB with a
length of 0.792 KB. (32) The gene that has the name abrb. The
genomic start and stop positions of this gene are 747.037 KB and
745.946 KB with a length of 1.092 KB. (33) The gene that has the

name ybgo. The genomic start and stop positions of this gene are 748.930 KB and 747.144 KB with a length of 1.787 KB. (34) The gene that has the name ybgq. The genomic start and stop positions of this gene are 751.401 KB and 748.945 KB with a length of 2.457 KB. (35) The gene that has the name ybgd. The genomic start and stop positions of this gene are 752.018 KB and 751.452 KB with a length of 0.567 KB. (36) The gene that has the name glta and with a COG identifier of COG0372. The genomic start and stop positions of this gene are 753.691 KB and 752.408 KB with a length of 1.284 KB. (37) The gene that has the name sdhc and with a COG identifier of COG2009. The genomic start and stop positions of this gene are 754.400 KB and 756.896 KB with a length of 2.497 KB. (38) The gene that has the name sdhb and with a COG identifier of COG0479. The genomic start and stop positions of this gene are 756.912 KB and 757.628 KB with a length of 0.717 KB. (39) The gene that has the name b0725. The genomic start and stop positions of this gene are 757.687 KB and 760.730 KB with a length of 3.044 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 816 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.055 KB and 707.109 KB with a length of 0.055 KB. (2) The connectron that has the identifier 819 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.112 KB and 707.162 KB with a length of 0.051 KB. (3) The connectron that has the identifier 823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 710.647 KB and 710.633 KB with a length of 0.015 KB. (4) The connectron that has the identifier 825 is on chromosome 1 in the negative direction. The

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genomic start and stop positions of this connectron are 710.666
KB and 710.652 KB with a length of 0.015 KB. (5) The connectron
that has the identifier 830 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this

5   connectron are 714.481 KB and 714.519 KB with a length of 0.039
KB. (6) The connectron that has the identifier 832 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 714.524 KB and 714.540 KB
with a length of 0.017 KB. (7) The connectron that has the

10   identifier 835 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 714.593
KB and 714.543 KB with a length of 0.051 KB. (8) The connectron
that has the identifier 838 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this

15   connectron are 714.544 KB and 714.606 KB with a length of 0.063
KB. (9) The connectron that has the identifier 844 is on
chromosome 1 in the negative direction. The genomic start and
stop positions of this connectron are 720.296 KB and 720.278 KB
with a length of 0.019 KB. (10) The connectron that has the

20   identifier 852 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 729.408
KB and 729.446 KB with a length of 0.039 KB. (11) The connectron
that has the identifier 854 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this

25   connectron are 730.443 KB and 730.457 KB with a length of 0.015
KB. (12) The connectron that has the identifier 855 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 730.468 KB and 730.482 KB
with a length of 0.015 KB. (13) The connectron that has the

30   identifier 856 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 730.484
KB and 730.507 KB with a length of 0.024 KB. (14) The connectron

that has the identifier 857 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.251 KB and 731.290 KB with a length of 0.040 KB. (15) The connectron that has the identifier 865 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.994 KB and 732.016 KB with a length of 0.023 KB. (16) The connectron that has the identifier 866 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.019 KB and 732.034 KB with a length of 0.016 KB. (17) The connectron that has the identifier 869 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.065 KB and 732.179 KB with a length of 0.115 KB. (18) The connectron that has the identifier 870 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.198 KB and 732.212 KB with a length of 0.015 KB. (19) The connectron that has the identifier 872 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.214 KB and 732.233 KB with a length of 0.020 KB. (20) The connectron that has the identifier 874 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.235 KB and 732.283 KB with a length of 0.049 KB. (21) The connectron that has the identifier 876 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.306 KB and 732.326 KB with a length of 0.021 KB. (22) The connectron that has the identifier 878 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.328 KB and 732.452 KB with a length of 0.125 KB. (23) The connectron that has the identifier 880 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

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connectron are 732.454 KB and 732.482 KB with a length of 0.029 KB. (24) The connectron that has the identifier 881 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.488 KB and 732.519 KB with a length of 0.032 KB. (25) The connectron that has the identifier 892 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.865 KB and 733.887 KB with a length of 0.023 KB. (26) The connectron that has the identifier 893 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.890 KB and 733.905 KB with a length of 0.016 KB. (27) The connectron that has the identifier 895 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.936 KB and 734.050 KB with a length of 0.115 KB. (28) The connectron that has the identifier 897 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.052 KB and 734.139 KB with a length of 0.088 KB. (29) The connectron that has the identifier 900 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.164 KB and 734.321 KB with a length of 0.158 KB. (30) The connectron that has the identifier 903 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.323 KB and 734.381 KB with a length of 0.059 KB. (31) The connectron that has the identifier 904 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.525 KB and 735.569 KB with a length of 0.045 KB. (32) The connectron that has the identifier 906 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.606 KB and 735.703 KB with a length of 0.098 KB. (33) The connectron that has the identifier 909 is on

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chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.707 KB and 735.728 KB with a length of 0.022 KB. (34) The connectron that has the identifier 911 is on chromosome 1 in the positive direction. The

5 genomic start and stop positions of this connectron are 735.807 KB and 735.964 KB with a length of 0.158 KB. (35) The connectron that has the identifier 915 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.986 KB and 736.083 KB with a length of 0.098

10 KB. (36) The connectron that has the identifier 927 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.017 KB and 737.032 KB with a length of 0.016 KB. (37) The connectron that has the identifier 928 is on chromosome 1 in the positive direction. The

15 genomic start and stop positions of this connectron are 737.035 KB and 737.057 KB with a length of 0.023 KB. (38) The connectron that has the identifier 931 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.261 KB and 737.275 KB with a length of 0.015

20 KB. (39) The connectron that has the identifier 932 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.278 KB and 737.292 KB with a length of 0.015 KB. (40) The connectron that has the identifier 945 is on chromosome 1 in the positive direction. The

25 genomic start and stop positions of this connectron are 737.930 KB and 737.967 KB with a length of 0.038 KB. (41) The connectron that has the identifier 957 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 740.290 KB and 740.172 KB with a length of 0.119

30 KB. (42) The connectron that has the identifier 958 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 740.172 KB and 740.290 KB

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with a length of 0.119 KB. (43) The connectron that has the
identifier 965 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 744.643
KB and 744.657 KB with a length of 0.015 KB. (44) The connectron
that has the identifier 966 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this
connectron are 744.664 KB and 744.678 KB with a length of 0.015
KB. (45) The connectron that has the identifier 968 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 755.680 KB and 755.714 KB
with a length of 0.035 KB. (46) The connectron that has the
identifier 971 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 757.628
KB and 757.712 KB with a length of 0.085 KB. (47) The connectron
that has the identifier 974 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this
connectron are 757.717 KB and 757.736 KB with a length of 0.020
KB.

**Addition of a Synthetic Transient Connectron between chromosomes
– Type 7 from Table 2**

A synthetic virtual connectron of type 7 in which the C1 is a
synthetic element and C2 is a natural element, the T1 is a
natural element and the T2 is a synthetic element can be
introduced into the *S. cerevisiae* genome by modifying the DNA
double-strand sequence at 221.330kb through 221.345kb on
chromosome 2 for a length of 0.016kb and by modifying the DNA

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double-strand sequence at 488.140kb through 488.297 on
chromosome 5 for a length of 0.158kb.

To create this example of a synthetic connectron of type 7 the
5   T2 sequence for natural connectron 3558 (old position 497.581kb
through 498.091kb) was copied into the new position stated
above.

Connectron 75273 is an example of a transient connectron. It is
10   described as

Global_Id	Chromosome	C1/C2 C1_Id	C2_Id	Chromosome	T1-T2 T1_Id	T2_Id	Connectron_Type
75273	2	792a	793	5	4749	4824a	transient

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The C1/C2 source of the transient connectron 75273 is
represented in table 1 as

Type	Num Jobno	Chr	Start	Stop	Length	GeneName
CPT	792a 22	2	221.330	221.345	.016	-->
CPT	793 22	2	221.346	221.361	.016	-->

The "Type" descriptor of this transient C1/C2 connectron source
is "CPT". The letter "P" indicates that the C1/C2 connectron
25   source occurs on the positive strand of the double-stranded DNA
of the genome. The letter "N" in this place would indicate a
C1/C2 connectron source on the negative strand of the genomic
DNA. The letter "T" in this descriptor indicates a "transient"
connectron. Similarly, the letter "P" would indicate a
30   permanent connectron that is shown in a later example. The
"Start", "Stop" and "Length" descriptors throughout these
examples are given in kilo-bases (KB). The symbol OS-> occurs
because there is another connectron formed by this C1/C2 that
happens to be a one-shot connectron.

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The T1-T2 target of the transient connectron 75273 as shown in table 1 is represented as

	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
5	TN	4749	59	5	448.454	448.992	.539		*-*
	TP	4750	68	5	448.454	448.992	.539		*-+
	CNT	4751	64	5	448.454	448.992	.539		--> ǀ
	TP	4752	63	5	449.003	449.315	.313		*-+
10	TN	4753	65	5	449.003	449.315	.313		*-+
	CNT	4754	60	5	449.003	449.315	.313		OS-> ǀ
	CNT	4755	5	5	449.317	449.482	.166		OS-> ǀ
	TN	4756	5	5	449.317	449.482	.166		*-+
	TP	4757	64	5	449.317	449.482	.148		*-+
15	GG	4758	59	5	449.470	449.574	.105	Group0615	ǀ
	CPT	4759	70	5	449.490	449.563	.074		--> ǀ
	TN	4760	70	5	449.490	449.563	.074		*-+
	TP	4761	67	5	449.490	449.558	.069		*-+
	CNT	4762	70	5	449.490	449.563	.074		--> ǀ
20	TN	4763	59	5	449.575	449.603	.029		*-+
	TP	4764	59	5	449.575	449.603	.029		*-+
	GG	4765	59	5	450.558	453.230	2.672	Group0616	ǀ
	TP	4766	59	5	452.176	452.190	.015		*-+
	GG	4767	59	5	453.454	454.914	1.461	Group0617	ǀ
25	CNT	4768	20	5	453.909	453.923	.015		--> ǀ
	CNT	4769	20	5	453.928	453.942	.015		--> ǀ
	TP	4770	59	5	454.644	454.658	.015		*-+
	GG	4771	59	5	455.141	457.600	2.460	Group0618	ǀ
	TN	4772	66	5	456.316	456.331	.016		*-+
30	GG	4773	59	5	457.801	460.218	2.418	Group0619	ǀ
	TN	4774	66	5	460.340	460.355	.016		*-+
	GG	4775	59	5	460.521	466.020	5.500	Group0620	ǀ
	GP	4776	59	5	462.580	462.861	.282	LSM5	ǀ
	TN	4777	59	5	463.743	463.758	.016		*-+
35	TP	4778	59	5	463.743	463.758	.016		*-+
	CPT	4779	61	5	463.990	464.004	.015		--> ǀ
	CPT	4780	61	5	464.010	464.024	.015		--> ǀ
	TP	4781	59	5	465.739	465.754	.016		*-ǀ
	GG	4782	59	5	466.203	468.811	2.609	Group0621	ǀ
40	GP	4783	59	5	468.365	468.811	.447	SPI1	ǀ
	TP	4784	69	5	469.451	469.518	.059		*-+
	CNT	4785	67	5	469.451	469.530	.080		OS-> ǀ
	GG	4786	59	5	469.452	469.525	.074	Group0622	ǀ
	TN	4787	59	5	469.452	469.532	.081		*-+
45	CPT	4788	67	5	469.452	469.531	.080		--> ǀ
	GG	4789	59	5	469.681	472.419	2.739	Group0623	ǀ

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	Type	Id							
	TN	4790	20	5	471.772	471.786	.015		*-+
	TP	4791	20	5	471.772	471.786	.015		*-+
	GG	4792	59	5	472.652	482.843	10.192	Group0624		
	GP	4793	59	5	475.015	476.223	1.209	OXA1		
5	TP	4794	63	5	476.803	476.817	.015		*-+
	CPT	4795	60	5	478.412	478.426	.015	-->	
	CPT	4796	60	5	478.436	478.450	.015	-->	
	CNT	4797	47	5	481.782	481.812	.031	-->	
	TN	4798	20	5	482.192	482.206	.015		*-+
10	CNT	4799	67	5	482.676	482.690	.015	-->	
	CNT	4800	67	5	482.701	482.715	.015	-->	
	GG	4801	59	5	483.320	487.188	3.869	Group0625		
	GP	4802	59	5	484.783	487.188	2.406	SEC34		
	CNT	4803	61	5	485.099	485.113	.015	-->	
15	CNT	4804	61	5	485.119	485.134	.016	-->	
	TN	4805	64	5	487.041	487.056	.016		*-+
	GG	4806	59	5	487.326	487.397	.072	Group0626		
	CPT	4807	61	5	487.375	487.397	.023	-->	
	CPT	4808	61	5	487.400	487.415	.016	-->	
20	CNT	4809	34	5	487.830	487.848	.019	OS->	
	CPT	4810	62	5	487.830	487.848	.019	OS->	
	TP	4811	60	5	487.830	487.848	.019		*-+
	TN	4812	59	5	487.830	487.848	.019		*-+
	CNT	4813	34	5	487.850	488.016	.167	OS->	
25	CPT	4814	5	5	487.850	488.016	.167	OS->	
	TP	4815	5	5	487.850	488.016	.167		*-+
	TN	4816	64	5	487.850	488.016	.167		*-+
	CNT	4817	47	5	488.024	488.137	.114	OS->	
	CPT	4818	47	5	488.024	488.068	.045	-->	
30	TN	4819	34	5	488.024	488.067	.044		*-+
	TP	4820	34	5	488.024	488.067	.044		*-+
	CPT	4821	69	5	488.069	488.137	.069	OS->	
	TN	4822	67	5	488.069	488.122	.054		*-+
	TP	4823	59	5	488.069	488.085	.017		*-+
35	TP	4824	5	5	488.094	488.137	.044		*-+
	TN	4824a	5	5	488.140	488.297	.158		*-*

The "Type" descriptor of the T1 (Id number 4749) is "TN" showing
that is T1 target is on the negative strand of the double-
40   stranded genomic DNA. Because the T1 and the T2 targets have to
be on the same strand, the T2 target (Id number 4824a) also has
the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

```
Type        Num Jobno  Chr    Start      Stop    Length GeneName
TN           xx    1 1   278.386   279.148    .763            *---*
XX           xx    1 1   278.387   278.416    .030          *   @
XX           xx    1 1   278.421   278.450    .030          *   @
TP           xx    1 1   278.452   278.892    .441          *---*
```

Group0615 (Id number 4758) has the type descriptor "GG". The same is true for Group0626 (Id number 4806).

Group0615 through Group0626 are described in table 2 as

```
-----------------------------------------------------------------
Group0615

Gene_Name COG_Id         Chromosome Direction    Start      Stop    Length
YER138W-A  -                     5  positive    449.470   449.574     .105
-----------------------------------------------------------------
Group0616

Gene_Name COG_Id         Chromosome Direction    Start      Stop    Length
YER139C    -                     5  negative    450.558   451.238     .681
YER140W    -                     5  positive    451.560   453.230    1.671
-----------------------------------------------------------------
Group0617

Gene_Name COG_Id         Chromosome Direction    Start      Stop    Length
COX15      COG1612    O          5  positive    453.454   454.914    1.461
-----------------------------------------------------------------
Group0618

Gene_Name COG_Id         Chromosome Direction    Start      Stop    Length
MAG1       COG0122    L          5  negative    455.141   456.031     .891
```

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```
       DDI1          -                      5  positive  456.314  457.600   1.287
       ---------------------------------------------------------------------------
       Group0619

   5   Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
       UBP5          -                      5  negative  457.801  460.218   2.418
       ---------------------------------------------------------------------------
       Group0620

  10   Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
       FTR1       COG0672     P           5  negative  460.521  461.735   1.215
       LSM5       COG1958     K           5  positive  462.580  462.861    .282
       YER147C       -                   5  negative  462.963  464.837   1.875
       SPT15      COG2101     K           5  positive  465.298  466.020    .723
  15   ---------------------------------------------------------------------------
       Group0621

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
       PEA2          -                      5  negative  466.203  467.465   1.263
  20   SPI1          -                      5  positive  468.365  468.811    .447
       ---------------------------------------------------------------------------
       Group0622

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
  25                                         5  positive  469.452  469.525    .074
       ---------------------------------------------------------------------------
       Group0623

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
  30   UBP3          -                      5  negative  469.681  472.419   2.739
       ---------------------------------------------------------------------------
       Group0624

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
  35   YER152C    COG1167     K           5  negative  472.652  473.983   1.332
       PET122        -                   5  negative  474.036  474.800    .765
       OXA1       COG0706     N           5  positive  475.015  476.223   1.209
       BEM2          -                   5  negative  476.340  482.843   6.504
       ---------------------------------------------------------------------------
  40   Group0625

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
       YER156C       -                   5  negative  483.320  484.336   1.017
       SEC34         -                   5  positive  484.783  487.188   2.406
  45   ---------------------------------------------------------------------------
       Group0626

       Gene_Name  COG_Id          Chromosome  Direction   Start     Stop   Length
```

```
                          5   positive   487.326   487.397     .072
------------------------------------------------------------------------
```

All of the data for the transient connectron 75273 are pulled together in the following table that is the "terse" description of the connectron.

```
------------------------------------------------------------------------
```

Connectron Relationships - Global_Id   Type
                          75273   transient

```
Control Sequences - Direction  Chromosome  C1/C2_Id    Start    Stop  Length
                    positive         2        792a    221.330  221.345   .016
                    positive         2        793     221.346  221.361   .016
```

```
Trigger Gene - Name       COG_Id    Start    Stop  Length
            YBL005W-B  -          221.293  226.561  5.269
```

```
Target Sequences  - Direction  Chromosome   T1_Id     Start    Stop  Length
                    negative         5        4749    448.992  448.454   .539

                                             T2_Id     Start    Stop  Length
                                             4824a    488.140  488.297   .158
```

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	5	Group0615	YER138W-A	-	positive	449.470	449.574	.105
2	5	Group0616	YER139C	-	positive	450.558	453.230	2.673
3	5	Group0616	YER140W	-	positive	451.560	453.230	1.671
4	5	Group0617	COX15	COG1612	positive	453.454	454.914	1.461
5	5	Group0618	MAG1	COG0122	positive	455.141	457.600	2.459
6	5	Group0618	DDI1	-	positive	456.314	457.600	1.287
7	5	Group0619	UBP5	-	positive	457.801	460.218	2.418
8	5	Group0620	FTR1	COG0672	positive	460.521	466.020	5.499
9	5	Group0620	LSM5	COG1958	positive	462.580	462.861	.282
10	5	Group0620	YER147C	-	negative	464.837	462.963	1.875
11	5	Group0620	SPT15	COG2101	positive	465.298	466.020	.723
12	5	Group0621	PEA2	-	positive	466.203	468.811	2.608
13	5	Group0621	SPI1	-	positive	468.365	468.811	.447
14	5	Group0622			positive	469.452	469.525	.074
15	5	Group0623	UBP3	-	positive	469.681	472.419	2.739
16	5	Group0624	YER152C	COG1167	positive	472.652	482.843	10.191
17	5	Group0624	PET122	-	negative	474.800	474.036	.765
18	5	Group0624	OXA1	COG0706	positive	475.015	476.223	1.209
19	5	Group0624	BEM2	-	negative	482.843	476.340	6.504

20	5	Group0625	YER156C	–	positive	483.320	487.188	3.868
21	5	Group0625	SEC34	–	positive	484.783	487.188	2.406
22	5	Group0626			positive	487.326	487.397	.072

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	5	4751	negative	448.992	448.454	.539
2	5	4754	negative	449.315	449.003	.313
3	5	4755	negative	449.482	449.317	.166
4	5	4759	positive	449.490	449.563	.074
5	5	4762	negative	449.563	449.490	.074
6	5	4768	negative	453.923	453.909	.015
7	5	4769	negative	453.942	453.928	.015
8	5	4779	positive	463.990	464.004	.015
9	5	4780	positive	464.010	464.024	.015
10	5	4785	negative	469.530	469.451	.080
11	5	4788	positive	469.452	469.531	.080
12	5	4795	positive	478.412	478.426	.015
13	5	4796	positive	478.436	478.450	.015
14	5	4797	negative	481.812	481.782	.031
15	5	4799	negative	482.690	482.676	.015
16	5	4800	negative	482.715	482.701	.015
17	5	4803	negative	485.113	485.099	.015
18	5	4804	negative	485.134	485.119	.016
19	5	4807	positive	487.375	487.397	.023
20	5	4808	positive	487.400	487.415	.016
21	5	4809	negative	487.848	487.830	.019
22	5	4810	positive	487.830	487.848	.019
23	5	4813	negative	488.016	487.850	.167
24	5	4814	positive	487.850	488.016	.167
25	5	4817	negative	488.137	488.024	.114
26	5	4818	positive	488.024	488.068	.045
27	5	4821	positive	488.069	488.137	.069

The verbose description of the transient connectron 75273 is:

In the Saccharomyces cerevisiae complete genome the transient connectron number 75273 is generated by the control sequence C1 whose identifier number is 792a. This control sequence is on the positive strand of the genomic DNA of chromosome 2. The genomic start and stop positions of this control sequence are 221.330 KB and 221.345 KB with a length of 0.016 KB and by the control

sequence C2 whose identifier number is 793. This control
sequence is on the positive strand of the genomic DNA of
chromosome 2. The genomic start and stop positions of this
control sequence are 221.346 KB and 221.361 KB with a length of

5   0.016 KB. Expression of the RNA for this connectron is triggered
by the promotion of the gene whose name is YBL005W-B. The
genomic start and stop positions of this gene are 221.293 KB and
226.561 KB and with a length of 5.269 KB. This connectron causes
stabilization of a loop of DNA. The target sequences (T1-T2)

10   are on the negative strand of the genomic DNA on chromosome 5.
The identifier number of the initiating target sequence (T1) is
4749. The genomic start and stop positions of this initiating
target sequence are 448.992 KB and 448.454 KB with a length of
0.022 KB. The identifier number of the terminating target

15   sequence (T2) is 4824a. The genomic start and stop positions of
this terminating target sequence are 488.140 KB and 488.297 KB
with a length of 0.158 KB.

This connectron controls the modulation of the expression of the
20   following gene(s): (1) The gene that has the name YER138W-A.
The genomic start and stop positions of this gene are 449.470 KB
and 449.574 KB with a length of 0.105 KB. (2) The gene that has
the name YER139C. The genomic start and stop positions of this
gene are 450.558 KB and 453.230 KB with a length of 2.672 KB.

25   (3) The gene that has the name YER140W. The genomic start and
stop positions of this gene are 451.560 KB and 453.230 KB with a
length of 1.671 KB. (4) The gene that has the name COX15 and
with a COG identifier of COG1612. The genomic start and stop
positions of this gene are 453.454 KB and 454.914 KB with a

30   length of 1.461 KB. (5) The gene that has the name MAG1 and with
a COG identifier of COG0122. The genomic start and stop
positions of this gene are 455.141 KB and 457.600 KB with a

length of 2.459 KB. (6) The gene that has the name DDI1. The genomic start and stop positions of this gene are 456.314 KB and 457.600 KB with a length of 1.287 KB. (7) The gene that has the name UBP5. The genomic start and stop positions of this gene are 457.801 KB and 460.218 KB with a length of 2.418 KB. (8) The gene that has the name FTR1 and with a COG identifier of COG0672. The genomic start and stop positions of this gene are 460.521 KB and 466.020 KB with a length of 5.499 KB. (9) The gene that has the name LSM5 and with a COG identifier of COG1958. The genomic start and stop positions of this gene are 462.580 KB and 462.861 KB with a length of 0.282 KB. (10) The gene that has the name YER147C. The genomic start and stop positions of this gene are 464.837 KB and 462.963 KB with a length of 1.875 KB. (11) The gene that has the name SPT15 and with a COG identifier of COG2101. The genomic start and stop positions of this gene are 465.298 KB and 466.020 KB with a length of 0.723 KB. (12) The gene that has the name PEA2. The genomic start and stop positions of this gene are 466.203 KB and 468.811 KB with a length of 2.608 KB. (13) The gene that has the name SPI1. The genomic start and stop positions of this gene are 468.365 KB and 468.811 KB with a length of 0.447 KB. (14) The gene that has the name No_Name. The genomic start and stop positions of this gene are 469.452 KB and 469.525 KB with a length of 0.074 KB. (15) The gene that has the name UBP3. The genomic start and stop positions of this gene are 469.681 KB and 472.419 KB with a length of 2.739 KB. (16) The gene that has the name YER152C and with a COG identifier of COG1167. The genomic start and stop positions of this gene are 472.652 KB and 482.843 KB with a length of 10.191 KB. (17) The gene that has the name PET122. The genomic start and stop positions of this gene are 474.800 KB and 474.036 KB with a length of 0.765 KB. (18) The gene that has the name OXA1 and with a COG identifier of

COG0706. The genomic start and stop positions of this gene are 475.015 KB and 476.223 KB with a length of 1.209 KB. (19) The gene that has the name BEM2. The genomic start and stop positions of this gene are 482.843 KB and 476.340 KB with a length of 6.504 KB. (20) The gene that has the name YER156C. The genomic start and stop positions of this gene are 483.320 KB and 487.188 KB with a length of 3.868 KB. (21) The gene that has the name SEC34. The genomic start and stop positions of this gene are 484.783 KB and 487.188 KB with a length of 2.406 KB. (22) The gene that has the name No_Name. The genomic start and stop positions of this gene are 487.326 KB and 487.397 KB with a length of 0.072 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 4751 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 448.992 KB and 448.454 KB with a length of 0.539 KB. (2) The connectron that has the identifier 4754 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.315 KB and 449.003 KB with a length of 0.313 KB. (3) The connectron that has the identifier 4755 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.482 KB and 449.317 KB with a length of 0.166 KB. (4) The connectron that has the identifier 4759 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 449.490 KB and 449.563 KB with a length of 0.074 KB. (5) The connectron that has the identifier 4762 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.563 KB and 449.490 KB with a length of 0.074 KB. (6) The connectron that has the identifier 4768 is on

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chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 453.923 KB and 453.909 KB with a length of 0.015 KB. (7) The connectron that has the identifier 4769 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 453.942 KB and 453.928 KB with a length of 0.015 KB. (8) The connectron that has the identifier 4779 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 463.990 KB and 464.004 KB with a length of 0.015 KB. (9) The connectron that has the identifier 4780 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 464.010 KB and 464.024 KB with a length of 0.015 KB. (10) The connectron that has the identifier 4785 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 469.530 KB and 469.451 KB with a length of 0.080 KB. (11) The connectron that has the identifier 4788 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 469.452 KB and 469.531 KB with a length of 0.080 KB. (12) The connectron that has the identifier 4795 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 478.412 KB and 478.426 KB with a length of 0.015 KB. (13) The connectron that has the identifier 4796 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 478.436 KB and 478.450 KB with a length of 0.015 KB. (14) The connectron that has the identifier 4797 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 481.812 KB and 481.782 KB with a length of 0.031 KB. (15) The connectron that has the identifier 4799 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 482.690 KB and 482.676 KB

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with a length of 0.015 KB. (16) The connectron that has the identifier 4800 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 482.715 KB and 482.701 KB with a length of 0.015 KB. (17) The connectron that has the identifier 4803 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 485.113 KB and 485.099 KB with a length of 0.015 KB. (18) The connectron that has the identifier 4804 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 485.134 KB and 485.119 KB with a length of 0.016 KB. (19) The connectron that has the identifier 4807 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.375 KB and 487.397 KB with a length of 0.023 KB. (20) The connectron that has the identifier 4808 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.400 KB and 487.415 KB with a length of 0.016 KB. (21) The connectron that has the identifier 4809 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 487.848 KB and 487.830 KB with a length of 0.019 KB. (22) The connectron that has the identifier 4810 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.830 KB and 487.848 KB with a length of 0.019 KB. (23) The connectron that has the identifier 4813 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 488.016 KB and 487.850 KB with a length of 0.167 KB. (24) The connectron that has the identifier 4814 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.850 KB and 488.016 KB with a length of 0.022 KB. (25) The connectron that has the identifier 4817 is on chromosome 5 in the negative direction.

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The genomic start and stop positions of this connectron are 488.137 KB and 488.024 KB with a length of 0.114 KB. (26) The connectron that has the identifier 4818 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 488.024 KB and 488.068 KB with a length of 0.045 KB. (27) The connectron that has the identifier 4821 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 488.069 KB and 488.137 KB with a length of 0.069 KB.

Addition of a Synthetic Connectron of Type 14 from Table 2

A synthetic virtual connectron of type 14 in which the C1 and C2 are natural elements, the T1 is a synthetic element and the T2 is a natual element can be introduced into the *Halobacterium sp.* genome by modifying the DNA double-strand sequences at 734.750kb through 734.942kb for a length of 0.193kb.

To create this example of a synthetic connectron of type 15 the T1 sequence for natural connectron 6627 (old position 733.018kb through 733.210kb) was copied into the new position stated above.

Connectron 7341 is an example of a transient connectron. It is described as

Global_Id	Chromosome	C1/C2 C1_Id	C2_Id	Chromosome	T1-T2 T1_Id	T2_Id	Connectron_Type
2587	1	6612	6612	1	6627	6852	transient

The C1/C2 source of the transient connectron 7341 is represented
in Table 1 as

```
     Type      Num Jobno  Chr   Start      Stop    Length GeneName
5    CPT      6612    1  1   732.401    732.534     .134     OS->  |||||||||||||||||||||||||||||||||
```

The "Type" descriptor of this transient C1/C2 connectron source
is "CPT". The letter "P" indicates that the C1/C2 connectron
source occurs on the positive strand of the double-stranded DNA
of the genome. The letter "N" in this place would indicate a
C1/C2 connectron source on the negative strand of the genomic
DNA. The letter "T" in this descriptor indicates a "transient"
connectron. Similarly, the letter "P" would indicate a
permanent connectron that is shown in a later example. The
"Start", "Stop" and "Length" descriptors throughout these
examples are given in kilo-bases (KB). The symbol OS-> occurs
because there is another connectron formed by this C1/C2 that
happens to be a one-shot connectron.

The T1-T2 target of the transient connectron 7341 as shown in
Table 1 is represented as

```
     Type      Num Jobno  Chr   Start      Stop    Length GeneName
     TP       6644a   1  1   734.750    734.942     .193            *-*
25   GG       6646    1  1   735.009    735.881     .873  Group0493   |
     CNT      6647    1  1   735.364    735.378     .015          OS->  |
     TN       6648    1  1   735.364    735.378     .015            *-+
     CNT      6649    1  1   735.389    735.403     .015          -->  |
     CNT      6650    1  1   735.753    735.767     .015          -->  |
30   CNT      6651    1  1   735.775    735.789     .015          -->  |
     GG       6652    1  1   735.910    737.544   1.634  Group0494   |
     TN       6653    1  1   735.969    735.984     .016            *-+
     TN       6654    1  1   736.126    736.140     .015            *-+
     CPT      6655    1  1   736.325    736.339     .015          -->  |
35   TN       6656    1  1   736.327    736.342     .016            *-+
     CPT      6657    1  1   736.345    736.359     .015          -->  |
     TP       6658    1  1   736.903    736.917     .015            *-+
     TN       6659    1  1   737.233    737.247     .015            *-+
```

	TP	6660	1	1	737.271	737.285	.015	*-+
	TN	6661	1	1	737.331	737.346	.016	*-+
	GG	6662	1	1	737.643	737.972	.330 Group0495 |
	TN	6663	1	1	737.752	737.766	.015	*-+
5	CNT	6664	1	1	737.752	737.782	.031	--> |
	TP	6665	1	1	737.761	737.775	.015	*-+
	TN	6666	1	1	738.049	738.063	.015	*-+
	GG	6667	1	1	738.107	739.835	1.728 Group0496 |
	TN	6668	1	1	738.122	738.136	.015	*-+
10	TP	6669	1	1	738.122	738.136	.015	*-+
	TP	6670	1	1	738.425	738.439	.015	*-+
	TP	6671	1	1	738.503	738.517	.015	*-+
	CNT	6672	1	1	738.517	738.562	.046	--> |
	TN	6673	1	1	738.544	738.559	.016	*-+
15	TN	6674	1	1	738.862	738.878	.017	*-+
	TP	6675	1	1	738.862	738.878	.017	*-+
	CNT	6676	1	1	738.975	738.989	.015	--> |
	CNT	6677	1	1	738.992	739.007	.016	--> |
	TN	6678	1	1	739.107	739.122	.016	*-+
20	GN	6679	1	1	739.248	739.835	.588 cheCl |
	TP	6680	1	1	739.435	739.449	.015	*-+
	TN	6681	1	1	739.685	739.707	.023	*-+
	TN	6682	1	1	739.761	739.775	.015	*-+
	GG	6683	1	1	739.838	741.844	2.007 Group0497 |
25	TN	6684	1	1	739.849	739.863	.015	*-+
	TP	6685	1	1	740.345	740.360	.016	*-+
	TN	6686	1	1	740.362	740.376	.015	*-+
	TP	6687	1	1	740.611	740.625	.015	*-+
	TN	6688	1	1	741.100	741.116	.017	*-+
30	TP	6689	1	1	741.101	741.132	.032	*-+
	TN	6690	1	1	741.218	741.232	.015	*-+
	CNT	6691	1	1	741.352	741.368	.017	--> |
	TP	6692	1	1	741.354	741.376	.023	*-+
	TN	6693	1	1	741.354	741.380	.027	*-+
35	CNT	6694	1	1	741.374	741.388	.015	--> |
	TN	6695	1	1	741.401	741.417	.017	*-+
	CNT	6696	1	1	741.519	741.533	.015	--> |
	CNT	6697	1	1	741.538	741.552	.015	--> |
	TN	6698	1	1	741.538	741.552	.015	*-+
40	TN	6699	1	1	741.561	741.575	.015	*-+
	GG	6700	1	1	741.846	743.248	1.403 Group0498 |
	TN	6701	1	1	741.924	741.942	.019	*-+
	TN	6702	1	1	742.194	742.208	.015	*-+
	TP	6703	1	1	742.618	742.632	.015	*-+
45	TN	6704	1	1	742.943	742.957	.015	*-+
	GG	6705	1	1	743.295	743.831	.537 Group0499 |
	TP	6706	1	1	743.730	743.748	.019	*-+
	GG	6707	1	1	743.896	744.489	.594 Group0500 |

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	TN	6708	1	1	743.916	743.930	.015	*-+
	GG	6709	1	1	744.606	745.511	.906 Group0501	|
	TN	6710	1	1	744.950	744.964	.015	*-+
	TN	6711	1	1	745.047	745.061	.015	*-+
5	GG	6712	1	1	745.648	746.763	1.116 Group0502	|
	CPT	6713	1	1	745.865	745.879	.015	--> |
	TN	6714	1	1	745.865	745.879	.015	*-+
	CPT	6715	1	1	745.888	745.902	.015	--> |
	CPT	6716	1	1	746.140	746.155	.016	--> |
10	TN	6717	1	1	746.153	746.175	.023	*-+
	TP	6718	1	1	746.157	746.175	.019	*-+
	CPT	6719	1	1	746.162	746.176	.015	--> |
	TN	6720	1	1	746.229	746.243	.015	*-+
	CNT	6721	1	1	746.229	746.259	.031	--> |
15	TN	6722	1	1	746.271	746.285	.015	*-+
	TP	6723	1	1	746.356	746.380	.025	*-+
	TN	6724	1	1	746.361	746.380	.020	*-+
	TN	6725	1	1	746.386	746.400	.015	*-+
	CPT	6726	1	1	746.453	746.467	.015	--> |
20	TN	6727	1	1	746.453	746.472	.020	*-+
	TP	6728	1	1	746.457	746.475	.019	*-+
	CPT	6729	1	1	746.469	746.483	.015	--> |
	TP	6730	1	1	746.528	746.545	.018	*-+
	TN	6731	1	1	746.532	746.556	.025	*-+
25	GG	6732	1	1	746.843	748.851	2.008 Group0503	|
	CNT	6733	1	1	746.905	746.919	.015	--> |
	CNT	6734	1	1	746.927	746.941	.015	--> |
	GN	6735	1	1	747.151	748.605	1.455 VNG0983C	|
	TN	6736	1	1	747.260	747.274	.015	*-+
30	TP	6737	1	1	747.475	747.489	.015	*-+
	TN	6738	1	1	747.547	747.571	.025	*-+
	TN	6739	1	1	747.934	747.948	.015	*-+
	TP	6740	1	1	747.936	747.950	.015	*-+
	TN	6741	1	1	748.130	748.144	.015	*-+
35	TP	6742	1	1	749.157	749.172	.016	*-+
	TN	6743	1	1	749.375	749.389	.015	*-+
	GG	6744	1	1	749.392	759.277	9.885 Group0504	|
	CNT	6745	1	1	759.509	759.552	.044	--> |
	TP	6746	1	1	759.509	760.014	.506	*-+
40	TN	6747	1	1	759.528	760.031	.504	*-+
	GG	6748	1	1	759.667	762.487	2.820 Group0505	|
	GP	6749	1	1	760.682	762.487	1.806 boa4	|
	CPT	6750	1	1	760.774	760.789	.016	--> |
	CPT	6751	1	1	760.798	760.814	.017	--> |
45	TN	6752	1	1	760.875	760.889	.015	*-+
	CPT	6753	1	1	760.878	760.892	.015	--> |
	CPT	6754	1	1	760.897	760.912	.016	--> |
	CPT	6755	1	1	761.496	761.510	.015	--> |

```
     CPT    6756    1  1   761.516   761.533    .018      -->  |
     CPT    6757    1  1   761.542   761.557    .016      -->  |
     TN     6758    1  1   761.542   761.557    .016         *-+
     CPT    6759    1  1   761.576   761.597    .022      -->  |
 5   CPT    6760    1  1   761.601   761.617    .017      -->  |
     TN     6761    1  1   761.754   761.768    .015         *-+
     CPT    6762    1  1   761.933   761.950    .018      -->  |
     TP     6763    1  1   761.933   761.950    .018         *-+
     CPT    6764    1  1   761.953   761.968    .016      -->  |
10   TN     6765    1  1   762.423   762.437    .015         *-+
     GG     6766    1  1   762.609   764.612   2.004  Group0506   |
     TN     6767    1  1   762.874   762.900    .027         *-+
     TN     6768    1  1   762.946   762.960    .015         *-+
     TN     6769    1  1   763.108   763.122    .015         *-+
15   TN     6770    1  1   763.273   763.304    .032         *-+
     CPT    6771    1  1   763.283   763.304    .022      -->  |
     TN     6772    1  1   763.306   763.320    .015         *-+
     CPT    6773    1  1   763.306   763.321    .016      -->  |
     CPT    6774    1  1   763.346   763.360    .015      -->  |
20   TN     6775    1  1   763.351   763.365    .015         *-+
     TP     6776    1  1   763.351   763.365    .015         *-+
     CPT    6777    1  1   763.362   763.376    .015      -->  |
     TP     6778    1  1   763.391   763.407    .017         *-+
     TN     6779    1  1   763.843   763.857    .015         *-+
25   TP     6780    1  1   763.843   763.857    .015         *-+
     CNT    6781    1  1   763.965   763.986    .022      -->  |
     CPT    6782    1  1   763.965   763.995    .031      -->  |
     CNT    6783    1  1   763.990   764.011    .022      -->  |
     CPT    6784    1  1   764.000   764.015    .016      -->  |
30   CNT    6785    1  1   764.075   764.089    .015      -->  |
     CNT    6786    1  1   764.093   764.108    .016      -->  |
     CPT    6787    1  1   764.156   764.171    .016      -->  |
     CNT    6788    1  1   764.156   764.177    .022     OS->  |
     TN     6789    1  1   764.156   764.177    .022         *-+
35   CNT    6790    1  1   764.181   764.195    .015      -->  |
     TP     6791    1  1   764.181   764.201    .021         *-+
     CPT    6792    1  1   764.181   764.204    .024      -->  |
     CPT    6793    1  1   764.213   764.227    .015      -->  |
     TP     6794    1  1   764.309   764.328    .020         *-+
40   TN     6795    1  1   764.312   764.326    .015         *-+
     TN     6796    1  1   764.383   764.397    .015         *-+
     TP     6797    1  1   764.530   764.545    .016         *-+
     TN     6798    1  1   764.530   764.548    .019         *-+
     GG     6799    1  1   764.619   765.629   1.011  Group0507   |
45   CPT    6800    1  1   764.791   764.808    .018      -->  |
     CNT    6801    1  1   764.794   764.813    .020     OS->  |
     TN     6802    1  1   764.794   764.832    .039         *-+
     CPT    6803    1  1   764.810   764.826    .017      -->  |
```

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	CNT	6804	1	1	764.818	764.832	.015	-->	
	CPT	6805	1	1	764.831	764.853	.023	-->	
	CPT	6806	1	1	764.856	764.870	.015	-->	
	CNT	6807	1	1	764.984	764.998	.015	OS->	
5	TN	6808	1	1	764.984	765.014	.031	*-+	
	CNT	6809	1	1	765.000	765.014	.015	-->	
	TN	6810	1	1	765.075	765.089	.015	*-+	
	CNT	6811	1	1	765.431	765.446	.016	-->	
	CNT	6812	1	1	765.456	765.473	.018	-->	
10	CNT	6813	1	1	765.479	765.494	.016	-->	
	TN	6814	1	1	765.508	765.523	.016	*-+	
	TP	6815	1	1	765.573	765.587	.015	*-+	
	GG	6816	1	1	765.775	766.044	.270	Group0508	
	TN	6817	1	1	765.822	765.837	.016	*-+	
15	TP	6818	1	1	766.162	766.176	.015	*-+	
	TN	6819	1	1	766.432	766.447	.016	*-+	
	GG	6820	1	1	766.603	766.812	.210	Group0509	
	CNT	6821	1	1	766.635	766.653	.019	OS->	
	TN	6822	1	1	766.635	766.653	.019	*-+	
20	CNT	6823	1	1	766.655	766.675	.021	-->	
	TN	6824	1	1	766.863	766.878	.016	*-+	
	GG	6825	1	1	766.955	768.538	1.584	Group0510	
	TN	6826	1	1	767.682	767.700	.019	*-+	
	TP	6827	1	1	767.831	767.845	.015	*-+	
25	TN	6828	1	1	768.028	768.048	.021	*-+	
	TP	6829	1	1	768.033	768.049	.017	*-+	
	TN	6830	1	1	768.377	768.391	.015	*-+	
	GG	6831	1	1	768.965	769.882	.918	Group0511	
	TN	6832	1	1	769.502	769.516	.015	*-+	
30	TN	6833	1	1	769.541	769.555	.015	*-+	
	TP	6834	1	1	769.559	769.573	.015	*-+	
	GG	6835	1	1	769.965	770.189	.225	Group0512	
	TN	6836	1	1	770.120	770.134	.015	*-+	
	GG	6837	1	1	770.194	770.406	.213	Group0513	
35	CPT	6838	1	1	770.226	770.240	.015	-->	
	CPT	6839	1	1	770.251	770.265	.015	-->	
	TP	6840	1	1	770.251	770.268	.018	*-+	
	CPT	6841	1	1	770.347	770.363	.017	-->	
	CPT	6842	1	1	770.365	770.379	.015	-->	
40	GG	6843	1	1	770.516	771.546	1.030	Group0514	
	TN	6844	1	1	771.564	772.071	.508	*-+	
	CNT	6845	1	1	771.564	772.086	.523	-->	
	TP	6846	1	1	771.583	772.084	.502	*-+	
	GG	6847	1	1	771.722	771.925	.204	Group0515	
45	TN	6848	1	1	772.963	772.977	.015	*-+	
	TP	6849	1	1	773.358	773.387	.030	*-+	
	GG	6850	1	1	773.360	773.950	.591	Group0516	
	CPT	6851	1	1	773.399	773.483	.085	OS->	

```
TP        6852    1 1   773.399  773.483    .085            *-*
```

The "Type" descriptor of the T1 (Id number 6644a) is "TP"
showing that is T1 target is on the negative strand of the
5   double-stranded genomic DNA. Because the T1 and the T2 targets
have to be on the same strand, the T2 target (Id number 6852)
also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path
10   from the * of the T1 to the right to the appropriate *, then by
tracing a path down the diagram to the first *, then by tracing
a path left to the * of the T2. When horizontal lines
(indicated by -) intersect with other vertical lines (indicated
by |) then the symbol at that point is changed to a +. When the
15   T1-T2 loop does not contain an groups of genes then the vertical
symbol (indicated by | or +) is changed to @ as shown below

```
     Type    Num Jobno  Chr   Start      Stop     Length GeneName
     TN      xx     1 1   278.386   279.148    .763            *---*
20   XX      xx     1 1   278.387   278.416    .030         *    @
     XX      xx     1 1   278.421   278.450    .030         *    @
     TP      xx     1 1   278.452   278.892    .441            *---*
```

Group0493 (Id number 6646) has the type descriptor "GG". The
25   same is true for the group headers through to Group0516 (Id
number 6847).

```
     ------------------------------------------------------------------
     Group0493
30
     Gene_Name    COG_Id          Chromosome  Direction    Start      Stop     Length
     VNG0964C     COG2469    S           1  positive    735.009   735.881    .873
     ------------------------------------------------------------------
     Group0494
35
     Gene_Name    COG_Id          Chromosome  Direction    Start      Stop     Length
     VNG0965C     COG2469    S           1  negative    735.910   736.773    .864
     cheR         COG1352    N           1  negative    736.840   737.544    .705
```
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```
----------------------------------------------------------------------
Group0495

       Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
  5    cheD       COG1871  N            1  negative  737.643  737.972     .330
----------------------------------------------------------------------
Group0496

       Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
 10    VNG0969H   COG1776  N            1  negative  738.107  739.246    1.140
       cheC1      COG1776  N            1  negative  739.248  739.835     .588
----------------------------------------------------------------------
Group0497

 15    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       cheA       COG0643  N            1  negative  739.838  741.844    2.007
----------------------------------------------------------------------
Group0498

 20    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       cheB       COG2201  N            1  negative  741.846  743.248    1.403
----------------------------------------------------------------------
Group0499

 25    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       cheW1      COG0835  N            1  negative  743.295  743.831     .537
----------------------------------------------------------------------
Group0500

 30    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       VNG0978H                        1  negative  743.896  744.489     .594
----------------------------------------------------------------------
Group0501

 35    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       VNG0979H                        1  positive  744.606  745.511     .906
----------------------------------------------------------------------
Group0502

 40    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       VNG0981C   COG0436  E            1  positive  745.648  746.763    1.116
----------------------------------------------------------------------
Group0503

 45    Gene_Name  COG_Id       Chromosome  Direction   Start     Stop    Length
       VNG0982C   COG1873  S            1  positive  746.843  747.133     .291
       VNG0983C   COG0618  R            1  negative  747.151  748.605    1.455
       tRNA-Lys                        1  positive  748.778  748.851     .074
```

```
          --------------------------------------------------------------
          Group0504

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  5       VNG0985H                           1  positive    749.392   751.398    2.007
          VNG0986H                           1  positive    752.276   752.803     .528
          VNG0987H                           1  positive    753.131   753.547     .417
          VNG0988H  ·                        1  positive    754.149   754.391     .243
          VNG0989C   COG0582    L            1  negative    754.459   755.481    1.023
  10      VNG0990H                           1  positive    756.010   756.183     .174
          VNG0991H                           1  negative    756.675   757.016     .342
          VNG0992H                           1  negative    757.409   758.119     .711
          VNG0993H                           1  positive    758.465   759.277     .813

          --------------------------------------------------------------
  15      Group0505

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
          VNG0994H                           1  negative    759.667   759.870     .204
          VNG0995H                           1  positive    760.365   760.553     .189
  20      boa4       COG3413    R            1  positive    760.682   762.487    1.806

          --------------------------------------------------------------
          Group0506

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  25      acs2       COG0365    I            1  positive    762.609   764.612    2.004

          --------------------------------------------------------------
          Group0507

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  30      yajO2      COG0667    C            1  negative    764.619   765.629    1.011

          --------------------------------------------------------------
          Group0508

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  35      VNG0999H                           1  negative    765.775   766.044     .270

          --------------------------------------------------------------
          Group0509

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  40      VNG1000H   COG3205    S            1  positive    766.603   766.812     .210

          --------------------------------------------------------------
          Group0510

          Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
  45      guaB       COG0516    F            1  negative    766.955   768.538    1.584

          --------------------------------------------------------------
          Group0511
```

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```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    VNG1002H                           1  positive   768.965   769.882     .918
    --------------------------------------------------------------------------
    Group0512
```

```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    VNG1003H                           1  positive   769.965   770.189     .225
    --------------------------------------------------------------------------
    Group0513
```

```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    VNG1005H                           1  negative   770.194   770.406     .213
    --------------------------------------------------------------------------
    Group0514
```

```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    tRNA-Trp                           1  positive   770.516   770.691     .176
    VNG1006H                           1  positive   770.827   771.546     .720
    --------------------------------------------------------------------------
    Group0515
```

```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    VNG1007H                           1  negative   771.722   771.925     .204
    --------------------------------------------------------------------------
    Group0516
```

```
    Gene_Name  COG_Id         Chromosome  Direction    Start      Stop    Length
    flaA1a     COG1681    N           1  positive   773.360   773.950     .591
    --------------------------------------------------------------------------
```

All of the data for the transient connectron 7341 are pulled together in the following table that is the "terse" description of the connectron.

```
    --------------------------------------------------------------------------

    Connectron Relationships - Global_Id   Type
                                  7341    transient

    Control Sequences - Direction  Chromosome  C1/C2_Id      Start      Stop   Length
                        positive            1      6612    732.401   732.534    .134

    Trigger Gene - Name       COG_Id      Start      Stop   Length
                   flaB1      COG1681    731.799   732.380    .582

    Target Sequences  - Direction  Chromosome      T1_Id      Start      Stop   Length
```

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```
                 positive          1      6644a   734.750   734.942    .193

                                       T2_Id     Start      Stop  Length
                                        6852   773.399   773.483    .085
```

5

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0493	VNG0964C	COG2469	positive	735.009	735.881	.873
2	1	Group0494	VNG0965C	COG2469	positive	735.910	737.544	1.634
3	1	Group0494	cheR	COG1352	negative	737.544	736.840	.705
4	1	Group0495	cheD	COG1871	positive	737.643	737.972	.330
5	1	Group0496	VNG0969H	COG1776	positive	738.107	739.835	1.728
6	1	Group0496	cheC1	COG1776	negative	739.835	739.248	.588
7	1	Group0497	cheA	COG0643	positive	739.838	741.844	2.007
8	1	Group0498	cheB	COG2201	positive	741.846	743.248	1.403
9	1	Group0499	cheW1	COG0835	positive	743.295	743.831	.537
10	1	Group0500	VNG0978H		positive	743.896	744.489	.594
11	1	Group0501	VNG0979H		positive	744.606	745.511	.906
12	1	Group0502	VNG0981C	COG0436	positive	745.648	746.763	1.116
13	1	Group0503	VNG0982C	COG1873	positive	746.843	748.851	2.008
14	1	Group0503	VNG0983C	COG0618	negative	748.605	747.151	1.455
15	1	Group0504	VNG0985H		positive	749.392	759.277	9.885
16	1	Group0504	VNG0986H		positive	752.276	752.803	.528
17	1	Group0504	VNG0987H		positive	753.131	753.547	.417
18	1	Group0504	VNG0988H		positive	754.149	754.391	.243
19	1	Group0504	VNG0989C	COG0582	negative	755.481	754.459	1.023
20	1	Group0504	VNG0990H		positive	756.010	756.183	.174
21	1	Group0504	VNG0991H		negative	757.016	756.675	.342
22	1	Group0504	VNG0992H		negative	758.119	757.409	.711
23	1	Group0504	VNG0993H		positive	758.465	759.277	.813
24	1	Group0505	VNG0994H		positive	759.667	762.487	2.820
25	1	Group0505	VNG0995H		positive	760.365	760.553	.189
26	1	Group0505	boa4	COG3413	positive	760.682	762.487	1.806
27	1	Group0506	acs2	COG0365	positive	762.609	764.612	2.004
28	1	Group0507	yajO2	COG0667	positive	764.619	765.629	1.011
29	1	Group0508	VNG0999H		positive	765.775	766.044	.270
30	1	Group0509	VNG1000H	COG3205	positive	766.603	766.812	.210
31	1	Group0510	guaB	COG0516	positive	766.955	768.538	1.584
32	1	Group0511	VNG1002H		positive	768.965	769.882	.918
33	1	Group0512	VNG1003H		positive	769.965	770.189	.225
34	1	Group0513	VNG1005H		positive	770.194	770.406	.213
35	1	Group0514	tRNA-Trp		positive	770.516	771.546	1.030
36	1	Group0514	VNG1006H		positive	770.827	771.546	.720
37	1	Group0515	VNG1007H		positive	771.722	771.925	.204
38	1	Group0516	flaAla	COG1681	positive	773.360	773.950	.591

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Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length

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	1	1	6644	positive	734.735	734.749	.015
	2	1	6647	negative	735.378	735.364	.015
	3	1	6649	negative	735.403	735.389	.015
	4	1	6650	negative	735.767	735.753	.015
5	5	1	6651	negative	735.789	735.775	.015
	6	1	6655	positive	736.325	736.339	.015
	7	1	6657	positive	736.345	736.359	.015
	8	1	6664	negative	737.782	737.752	.031
	9	1	6672	negative	738.562	738.517	.046
10	10	1	6676	negative	738.989	738.975	.015
	11	1	6677	negative	739.007	738.992	.016
	12	1	6691	negative	741.368	741.352	.017
	13	1	6694	negative	741.388	741.374	.015
	14	1	6696	negative	741.533	741.519	.015
15	15	1	6697	negative	741.552	741.538	.015
	16	1	6713	positive	745.865	745.879	.015
	17	1	6715	positive	745.888	745.902	.015
	18	1	6716	positive	746.140	746.155	.016
	19	1	6719	positive	746.162	746.176	.015
20	20	1	6721	negative	746.259	746.229	.031
	21	1	6726	positive	746.453	746.467	.015
	22	1	6729	positive	746.469	746.483	.015
	23	1	6733	negative	746.919	746.905	.015
	24	1	6734	negative	746.941	746.927	.015
25	25	1	6745	negative	759.552	759.509	.044
	26	1	6750	positive	760.774	760.789	.016
	27	1	6751	positive	760.798	760.814	.017
	28	1	6753	positive	760.878	760.892	.015
	29	1	6754	positive	760.897	760.912	.016
30	30	1	6755	positive	761.496	761.510	.015
	31	1	6756	positive	761.516	761.533	.018
	32	1	6757	positive	761.542	761.557	.016
	33	1	6759	positive	761.576	761.597	.022
	34	1	6760	positive	761.601	761.617	.017
35	35	1	6762	positive	761.933	761.950	.018
	36	1	6764	positive	761.953	761.968	.016
	37	1	6771	positive	763.283	763.304	.022
	38	1	6773	positive	763.306	763.321	.016
	39	1	6774	positive	763.346	763.360	.015
40	40	1	6777	positive	763.362	763.376	.015
	41	1	6781	negative	763.986	763.965	.022
	42	1	6782	positive	763.965	763.995	.031
	43	1	6783	negative	764.011	763.990	.022
	44	1	6784	positive	764.000	764.015	.016
45	45	1	6785	negative	764.089	764.075	.015
	46	1	6786	negative	764.108	764.093	.016
	47	1	6787	positive	764.156	764.171	.016
	48	1	6788	negative	764.177	764.156	.022

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49	1	6790	negative	764.195	764.181	.015
50	1	6792	positive	764.181	764.204	.024
51	1	6793	positive	764.213	764.227	.015
52	1	6800	positive	764.791	764.808	.018
53	1	6801	negative	764.813	764.794	.020
54	1	6803	positive	764.810	764.826	.017
55	1	6804	negative	764.832	764.818	.015
56	1	6805	positive	764.831	764.853	.023
57	1	6806	positive	764.856	764.870	.015
58	1	6807	negative	764.998	764.984	.015
59	1	6809	negative	765.014	765.000	.015
60	1	6811	negative	765.446	765.431	.016
61	1	6812	negative	765.473	765.456	.018
62	1	6813	negative	765.494	765.479	.016
63	1	6821	negative	766.653	766.635	.019
64	1	6823	negative	766.675	766.655	.021
65	1	6838	positive	770.226	770.240	.015
66	1	6839	positive	770.251	770.265	.015
67	1	6841	positive	770.347	770.363	.017
68	1	6842	positive	770.365	770.379	.015
69	1	6845	negative	772.086	771.564	.523
70	1	6851	positive	773.399	773.483	.085

The verbose description of the transient connectron 7341 is:

In the Halobacterium sp. NRC-1 complete genome the transient
connectron number 7341 is generated by the control sequence
(C1/C2) whose identifier number is 6612. This control sequence
is on the positive strand of the genomic DNA of chromosome 1.
The genomic start and stop positions of this control sequence
are 732.401 KB and 732.534 KB with a length of 0.134 KB.
Expression of the RNA for this connectron is triggered by the
promotion of the gene whose name is flaB1 and whose COG (Cluster
of Orthologous Genes) identifier is COG1681. The genomic start
and stop positions of this gene are 731.799 KB and 732.380 KB
and with a length of 0.582 KB. This connectron causes
stabilization of a loop of DNA. The target sequences (T1-T2)
are on the positive strand of the genomic DNA on chromosome 1.

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The identifier number of the initiating target sequence (T1) is 6644a. The genomic start and stop positions of this initiating target sequence are 734.750 KB and 734.942 KB with a length of 0.193 KB. The identifier number of the terminating target

5 sequence (T2) is 6852. The genomic start and stop positions of this terminating target sequence are 773.399 KB and 773.483 KB with a length of 0.085 KB.

This connectron controls the modulation of the expression of the

10 following gene(s): (1) The gene that has the name VNG0964C and with a COG identifier of COG2469. The genomic start and stop positions of this gene are 735.009 KB and 735.881 KB with a length of 0.873 KB. (2) The gene that has the name VNG0965C and with a COG identifier of COG2469. The genomic start and stop

15 positions of this gene are 735.910 KB and 737.544 KB with a length of 1.634 KB. (3) The gene that has the name cheR and with a COG identifier of COG1352. The genomic start and stop positions of this gene are 737.544 KB and 736.840 KB with a length of 0.705 KB. (4) The gene that has the name cheD and with

20 a COG identifier of COG1871. The genomic start and stop positions of this gene are 737.643 KB and 737.972 KB with a length of 0.330 KB. (5) The gene that has the name VNG0969H and with a COG identifier of COG1776. The genomic start and stop positions of this gene are 738.107 KB and 739.835 KB with a

25 length of 1.728 KB. (6) The gene that has the name cheC1 and with a COG identifier of COG1776. The genomic start and stop positions of this gene are 739.835 KB and 739.248 KB with a length of 0.588 KB. (7) The gene that has the name cheA and with a COG identifier of COG0643. The genomic start and stop

30 positions of this gene are 739.838 KB and 741.844 KB with a length of 2.007 KB. (8) The gene that has the name cheB and with a COG identifier of COG2201. The genomic start and stop

positions of this gene are 741.846 KB and 743.248 KB with a length of 1.403 KB. (9) The gene that has the name cheW1 and with a COG identifier of COG0835. The genomic start and stop positions of this gene are 743.295 KB and 743.831 KB with a length of 0.537 KB. (10) The gene that has the name VNG0978H. The genomic start and stop positions of this gene are 743.896 KB and 744.489 KB with a length of 0.594 KB. (11) The gene that has the name VNG0979H. The genomic start and stop positions of this gene are 744.606 KB and 745.511 KB with a length of 0.906 KB. (12) The gene that has the name VNG0981C and with a COG identifier of COG0436. The genomic start and stop positions of this gene are 745.648 KB and 746.763 KB with a length of 1.116 KB. (13) The gene that has the name VNG0982C and with a COG identifier of COG1873. The genomic start and stop positions of this gene are 746.843 KB and 748.851 KB with a length of 2.008 KB. (14) The gene that has the name VNG0983C and with a COG identifier of COG0618. The genomic start and stop positions of this gene are 748.605 KB and 747.151 KB with a length of 1.455 KB. (15) The gene that has the name VNG0985H. The genomic start and stop positions of this gene are 749.392 KB and 759.277 KB with a length of 9.885 KB. (16) The gene that has the name VNG0986H. The genomic start and stop positions of this gene are 752.276 KB and 752.803 KB with a length of 0.528 KB. (17) The gene that has the name VNG0987H. The genomic start and stop positions of this gene are 753.131 KB and 753.547 KB with a length of 0.417 KB. (18) The gene that has the name VNG0988H. The genomic start and stop positions of this gene are 754.149 KB and 754.391 KB with a length of 0.243 KB. (19) The gene that has the name VNG0989C and with a COG identifier of COG0582. The genomic start and stop positions of this gene are 755.481 KB and 754.459 KB with a length of 1.023 KB. (20) The gene that has the name VNG0990H. The genomic start and stop positions of this

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gene are 756.010 KB and 756.183 KB with a length of 0.174 KB.
(21) The gene that has the name VNG0991H. The genomic start and
stop positions of this gene are 757.016 KB and 756.675 KB with a
length of 0.342 KB. (22) The gene that has the name VNG0992H.
The genomic start and stop positions of this gene are 758.119 KB
and 757.409 KB with a length of 0.711 KB. (23) The gene that has
the name VNG0993H. The genomic start and stop positions of this
gene are 758.465 KB and 759.277 KB with a length of 0.813 KB.
(24) The gene that has the name VNG0994H. The genomic start and
stop positions of this gene are 759.667 KB and 762.487 KB with a
length of 2.820 KB. (25) The gene that has the name VNG0995H.
The genomic start and stop positions of this gene are 760.365 KB
and 760.553 KB with a length of 0.189 KB. (26) The gene that has
the name boa4 and with a COG identifier of COG3413. The genomic
start and stop positions of this gene are 760.682 KB and 762.487
KB with a length of 1.806 KB. (27) The gene that has the name
acs2 and with a COG identifier of COG0365. The genomic start
and stop positions of this gene are 762.609 KB and 764.612 KB
with a length of 2.004 KB. (28) The gene that has the name yajO2
and with a COG identifier of COG0667. The genomic start and
stop positions of this gene are 764.619 KB and 765.629 KB with a
length of 1.011 KB. (29) The gene that has the name VNG0999H.
The genomic start and stop positions of this gene are 765.775 KB
and 766.044 KB with a length of 0.270 KB. (30) The gene that has
the name VNG1000H and with a COG identifier of COG3205. The
genomic start and stop positions of this gene are 766.603 KB and
766.812 KB with a length of 0.210 KB. (31) The gene that has the
name guaB and with a COG identifier of COG0516. The genomic
start and stop positions of this gene are 766.955 KB and 768.538
KB with a length of 1.584 KB. (32) The gene that has the name
VNG1002H. The genomic start and stop positions of this gene are
768.965 KB and 769.882 KB with a length of 0.918 KB. (33) The

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gene that has the name VNG1003H. The genomic start and stop
positions of this gene are 769.965 KB and 770.189 KB with a
length of 0.225 KB. (34) The gene that has the name VNG1005H.
The genomic start and stop positions of this gene are 770.194 KB

5   and 770.406 KB with a length of 0.213 KB. (35) The gene that has
the name tRNA-Trp. The genomic start and stop positions of this
gene are 770.516 KB and 771.546 KB with a length of 1.030 KB.
(36) The gene that has the name VNG1006H. The genomic start and
stop positions of this gene are 770.827 KB and 771.546 KB with a

10   length of 0.720 KB. (37) The gene that has the name VNG1007H.
The genomic start and stop positions of this gene are 771.722 KB
and 771.925 KB with a length of 0.204 KB. (38) The gene that has
the name flaA1a and with a COG identifier of COG1681. The
genomic start and stop positions of this gene are 773.360 KB and

15   773.950 KB with a length of 0.591 KB.

This connectron controls the turning off of the expression of
the following connectron(s): (1) The connectron that has the
identifier 6644 is on chromosome 1 in the positive direction.

20   The genomic start and stop positions of this connectron are
734.735 KB and 734.749 KB with a length of 0.015 KB. (2) The
connectron that has the identifier 6647 is on chromosome 1 in
the negative direction. The genomic start and stop positions of
this connectron are 735.378 KB and 735.364 KB with a length of

25   0.015 KB. (3) The connectron that has the identifier 6649 is on
chromosome 1 in the negative direction. The genomic start and
stop positions of this connectron are 735.403 KB and 735.389 KB
with a length of 0.015 KB. (4) The connectron that has the
identifier 6650 is on chromosome 1 in the negative direction.

30   The genomic start and stop positions of this connectron are
735.767 KB and 735.753 KB with a length of 0.015 KB. (5) The
connectron that has the identifier 6651 is on chromosome 1 in

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the negative direction. The genomic start and stop positions of this connectron are 735.789 KB and 735.775 KB with a length of 0.015 KB. (6) The connectron that has the identifier 6655 is on chromosome 1 in the positive direction. The genomic start and

5   stop positions of this connectron are 736.325 KB and 736.339 KB with a length of 0.015 KB. (7) The connectron that has the identifier 6657 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 736.345 KB and 736.359 KB with a length of 0.015 KB. (8) The

10   connectron that has the identifier 6664 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 737.782 KB and 737.752 KB with a length of 0.031 KB. (9) The connectron that has the identifier 6672 is on chromosome 1 in the negative direction. The genomic start and

15   stop positions of this connectron are 738.562 KB and 738.517 KB with a length of 0.046 KB. (10) The connectron that has the identifier 6676 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 738.989 KB and 738.975 KB with a length of 0.015 KB. (11) The

20   connectron that has the identifier 6677 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 739.007 KB and 738.992 KB with a length of 0.016 KB. (12) The connectron that has the identifier 6691 is on chromosome 1 in the negative direction. The genomic start and

25   stop positions of this connectron are 741.368 KB and 741.352 KB with a length of 0.017 KB. (13) The connectron that has the identifier 6694 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.388 KB and 741.374 KB with à length of 0.015 KB. (14) The

30   connectron that has the identifier 6696 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.533 KB and 741.519 KB with a length of

0.015 KB. (15) The connectron that has the identifier 6697 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.552 KB and 741.538 KB with a length of 0.015 KB. (16) The connectron that has the identifier 6713 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 745.865 KB and 745.879 KB with a length of 0.015 KB. (17) The connectron that has the identifier 6715 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 745.888 KB and 745.902 KB with a length of 0.015 KB. (18) The connectron that has the identifier 6716 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.140 KB and 746.155 KB with a length of 0.016 KB. (19) The connectron that has the identifier 6719 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.162 KB and 746.176 KB with a length of 0.015 KB. (20) The connectron that has the identifier 6721 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 746.259 KB and 746.229 KB with a length of 0.031 KB. (21) The connectron that has the identifier 6726 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.453 KB and 746.467 KB with a length of 0.015 KB. (22) The connectron that has the identifier 6729 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.469 KB and 746.483 KB with a length of 0.015 KB. (23) The connectron that has the identifier 6733 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 746.919 KB and 746.905 KB with a length of 0.015 KB. (24) The connectron that has the identifier 6734 is on chromosome 1 in the negative direction. The genomic start and

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stop positions of this connectron are 746.941 KB and 746.927 KB with a length of 0.015 KB. (25) The connectron that has the identifier 6745 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 759.552 KB and 759.509 KB with a length of 0.044 KB. (26) The connectron that has the identifier 6750 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.774 KB and 760.789 KB with a length of 0.016 KB. (27) The connectron that has the identifier 6751 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.798 KB and 760.814 KB with a length of 0.017 KB. (28) The connectron that has the identifier 6753 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.878 KB and 760.892 KB with a length of 0.015 KB. (29) The connectron that has the identifier 6754 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.897 KB and 760.912 KB with a length of 0.016 KB. (30) The connectron that has the identifier 6755 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.496 KB and 761.510 KB with a length of 0.015 KB. (31) The connectron that has the identifier 6756 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.516 KB and 761.533 KB with a length of 0.018 KB. (32) The connectron that has the identifier 6757 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.542 KB and 761.557 KB with a length of 0.016 KB. (33) The connectron that has the identifier 6759 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.576 KB and 761.597 KB with a length of 0.022 KB. (34) The connectron that has the

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identifier 6760 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.601 KB and 761.617 KB with a length of 0.017 KB. (35) The connectron that has the identifier 6762 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.933 KB and 761.950 KB with a length of 0.018 KB. (36) The connectron that has the identifier 6764 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.953 KB and 761.968 KB with a length of 0.016 KB. (37) The connectron that has the identifier 6771 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.283 KB and 763.304 KB with a length of 0.022 KB. (38) The connectron that has the identifier 6773 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.306 KB and 763.321 KB with a length of 0.016 KB. (39) The connectron that has the identifier 6774 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.346 KB and 763.360 KB with a length of 0.015 KB. (40) The connectron that has the identifier 6777 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.362 KB and 763.376 KB with a length of 0.015 KB. (41) The connectron that has the identifier 6781 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 763.986 KB and 763.965 KB with a length of 0.022 KB. (42) The connectron that has the identifier 6782 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.965 KB and 763.995 KB with a length of 0.031 KB. (43) The connectron that has the identifier 6783 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are

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764.011 KB and 763.990 KB with a length of 0.022 KB. (44) The connectron that has the identifier 6784 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.000 KB and 764.015 KB with a length of

0.016 KB. (45) The connectron that has the identifier 6785 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.089 KB and 764.075 KB with a length of 0.015 KB. (46) The connectron that has the identifier 6786 is on chromosome 1 in the negative direction.

The genomic start and stop positions of this connectron are 764.108 KB and 764.093 KB with a length of 0.016 KB. (47) The connectron that has the identifier 6787 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.156 KB and 764.171 KB with a length of

0.016 KB. (48) The connectron that has the identifier 6788 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.177 KB and 764.156 KB with a length of 0.022 KB. (49) The connectron that has the identifier 6790 is on chromosome 1 in the negative direction.

The genomic start and stop positions of this connectron are 764.195 KB and 764.181 KB with a length of 0.015 KB. (50) The connectron that has the identifier 6792 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.181 KB and 764.204 KB with a length of

0.024 KB. (51) The connectron that has the identifier 6793 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.213 KB and 764.227 KB with a length of 0.015 KB. (52) The connectron that has the identifier 6800 is on chromosome 1 in the positive direction.

The genomic start and stop positions of this connectron are 764.791 KB and 764.808 KB with a length of 0.018 KB. (53) The connectron that has the identifier 6801 is on chromosome 1 in

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the negative direction. The genomic start and stop positions of this connectron are 764.813 KB and 764.794 KB with a length of 0.020 KB. (54) The connectron that has the identifier 6803 is on chromosome 1 in the positive direction. The genomic start and

5 stop positions of this connectron are 764.810 KB and 764.826 KB with a length of 0.017 KB. (55) The connectron that has the identifier 6804 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.832 KB and 764.818 KB with a length of 0.015 KB. (56) The

10 connectron that has the identifier 6805 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.831 KB and 764.853 KB with a length of 0.023 KB. (57) The connectron that has the identifier 6806 is on chromosome 1 in the positive direction. The genomic start and

15 stop positions of this connectron are 764.856 KB and 764.870 KB with a length of 0.015 KB. (58) The connectron that has the identifier 6807 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.998 KB and 764.984 KB with a length of 0.015 KB. (59) The

20 connectron that has the identifier 6809 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.014 KB and 765.000 KB with a length of 0.015 KB. (60) The connectron that has the identifier 6811 is on chromosome 1 in the negative direction. The genomic start and

25 stop positions of this connectron are 765.446 KB and 765.431 KB with a length of 0.016 KB. (61) The connectron that has the identifier 6812 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.473 KB and 765.456 KB with a length of 0.018 KB. (62) The

30 connectron that has the identifier 6813 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.494 KB and 765.479 KB with a length of

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0.016 KB. (63) The connectron that has the identifier 6821 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 766.653 KB and 766.635 KB with a length of 0.019 KB. (64) The connectron that has the

5   identifier 6823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 766.675 KB and 766.655 KB with a length of 0.021 KB. (65) The connectron that has the identifier 6838 is on chromosome 1 in the positive direction. The genomic start and stop positions of

10   this connectron are 770.226 KB and 770.240 KB with a length of 0.015 KB. (66) The connectron that has the identifier 6839 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.251 KB and 770.265 KB with a length of 0.015 KB. (67) The connectron that has the

15   identifier 6841 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.347 KB and 770.363 KB with a length of 0.017 KB. (68) The connectron that has the identifier 6842 is on chromosome 1 in the positive direction. The genomic start and stop positions of

20   this connectron are 770.365 KB and 770.379 KB with a length of 0.015 KB. (69) The connectron that has the identifier 6845 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 772.086 KB and 771.564 KB with a length of 0.523 KB. (70) The connectron that has the

25   identifier 6851 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 773.399 KB and 773.483 KB with a length of 0.085 KB.

30

Addition of a Synthetic Virtual Connectron of Type 15 from Table 2

5   A synthetic virtual connectron of type 15 in which the C1 and C2
       are natural elements, the T1 is a natural element and the T2 is
       a synthetic element can be introduced into the *P. aeruginosa*
       genome by modifying the DNA double-strand sequences at
       4838.155kb through 4838.323kb for a length of 0.169kb.
10
       To create this example of a synthetic connectron of type 14 the
       T2 sequence for natural connectron 23295 (old position
       4848.679kb through 4939.847kb) was copied into the new position
       stated above.
15
       Connectron 28739 is an example of a synthetic transient
       connectron. It is described as

20
Global_Id	Chromosome	C1/C2 C1_Id	C2_Id	Chromosome	T1-T2 T1_Id	T2_Id	Connectron_Type
28739	1	53464	53464	1	53531	53569	transient

       The C1/C2 source of the transient connectron 28739 is
25   represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
CPT	53464	1	1	4832.718	4832.838	.121	--> IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

30   The "Type" descriptor of this transient C1/C2 connectron source
       is "CPT". The letter "P" indicates that the C1/C2 connectron
       source occurs on the positive strand of the double-stranded DNA
       of the genome. The letter "N" in this place would indicate a

C1/C2 connectron source on the negative strand of the genomic
DNA. The letter "T" in this descriptor indicates a "transient"
connectron. Similarly, the letter "P" would indicate a
permanent connectron that is shown in a later example. The

5   "Start", "Stop" and "Length" descriptors throughout these
examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 28739 as shown in
table 1 is represented as

10

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TP	53531	1	1	4836.528	4836.721	.194	*-*
CPT	53532	1	1	4836.728	4836.746	.019	OS->	
TP	53533	1	1	4836.728	4836.746	.019	*-+
TN	53534	1	1	4836.728	4836.779	.052	*-+
CPT	53535	1	1	4836.748	4836.779	.032	OS->	
TP	53536	1	1	4836.748	4836.779	.032	*-+
CPT	53537	1	1	4836.781	4836.821	.041	OS->	
TP	53538	1	1	4836.781	4836.821	.041	*-+
TN	53539	1	1	4836.781	4836.918	.138	*-+
TP	53540	1	1	4836.840	4836.855	.016	*-+
CPT	53541	1	1	4836.877	4836.918	.042	OS->	
TP	53542	1	1	4836.877	4836.918	.042	*-+
TP	53543	1	1	4836.940	4836.957	.018	*-+
CPT	53544	1	1	4836.940	4836.982	.043	OS->	
CPT	53545	1	1	4836.990	4837.123	.134	OS->	
TP	53546	1	1	4836.990	4837.123	.134	*-+
TN	53547	1	1	4836.990	4837.153	.164	*-+
CPT	53548	1	1	4837.126	4837.148	.023	-->	
TP	53549	1	1	4837.129	4837.153	.025	*-+
TP	53549a	1	1	4838.155	4838.323	.169	*-*

The "Type" descriptor of the T1 (Id number 53531) is "TP"
showing that is T1 target is on the positive strand of the

35   double-stranded genomic DNA. Because the T1 and the T2 targets
have to be on the same strand, the T2 target (Id number 53549a)
also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

```
Type      Num Jobno  Chr   Start      Stop     Length GeneName
TN        xx    1  1   278.386    279.148    .763          *---*
XX        xx    1  1   278.387    278.416    .030          *    @
XX        xx    1  1   278.421    278.450    .030          *    @
TP        xx    1  1   278.452    278.892    .441          *---*
```

Since this synthetic connectron is a virtual connectron there are no gene groups that are controlled by the existence of this connectron. Instead the expression of the C1/C2 sources of six one-shot connectrons (type designator "CPT" for Id numbers 53532, 53535, 53537, 53541, 53544, and 53544) and one transient connectron (type designator "CPT" for Id numbers 53548) are controlled by this connectron.

All of the data for the transient connectron 28739 are pulled together in the following table that is the "terse" description of the connectron.

```
------------------------------------------------------------------------

Connectron Relationships - Global_Id   Type
                              28739   transient

Control Sequences - Direction  Chromosome  C1/C2_Id     Start      Stop   Length
                    positive            1  .  53464   4832.718  4832.838    .121

Trigger Gene - Name         COG_Id       Start      Stop  Length
               pctC        COG0840    4831.371  4833.269   1.899
```

```
       Target Sequences  - Direction Chromosome     T1_Id      Start       Stop  Length
                           positive          1      53531   4836.528   4836.721    .194


 5                                                    T2_Id      Start       Stop  Length
                                                     53549a   4838.155   4838.323    .169


       Controlled Genes
       none
10
       Controlled Connectrons
       Local_Id  Chromosome     C1/C2_Id   Direction      Start       Stop     Length
              1           1        53532    positive   4836.728   4836.746       .019
              2           1        53535    positive   4836.748   4836.779       .032
15            3           1        53537    positive   4836.781   4836.821       .041
              4           1        53541    positive   4836.877   4836.918       .042
              5           1        53544    positive   4836.940   4836.982       .043
              6           1        53545    positive   4836.990   4837.123       .134
              7           1        53548    positive   4837.126   4837.148       .023
20            8           1        53551    positive   4837.419   4837.448       .030
              9           1        53552    positive   4837.572   4837.622       .051
             10           1        53554    positive   4837.962   4837.999       .038
             11           1        53557    positive   4838.217   4838.258       .042
             12           1        53559    positive   4838.295   4838.362       .068
25           13           1        53563    positive   4838.457   4838.476       .020
             14           1        53564    positive   4838.478   4838.645       .168
             15           1        53567    positive   4838.654   4838.847       .194


       ------------------------------------------------------------------------
30
```

The verbose description of the transient connectron 28739 is:

In the Pseudomonas aeruginosa PA01, complete genome the transient connectron number 23295 is generated by the control sequence (C1/C2) whose identifier number is 53464. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 4832.718 KB and 4832.838 KB with a length of 0.121 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is pctC and whose COG (Cluster of Orthologous Genes) identifier is COG0840. The genomic start and stop positions of this gene are 4831.371

KB and 4833.269 KB and with a length of 1.899 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the positive strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is 53531. The genomic start and stop positions of this initiating target sequence are 4836.528 KB and 4836.721 KB with a length of 0.194 KB. The identifier number of the terminating target sequence (T2) is 53569. The genomic start and stop positions of this terminating target sequence are 4838.155 KB and 4838.323 KB with a length of 0.169 KB.

This connectron controls the modulation of the expression of the following gene(s): none

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 53532 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.728 KB and 4836.746 KB with a length of 0.019 KB. (2) The connectron that has the identifier 53535 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.748 KB and 4836.779 KB with a length of 0.032 KB. (3) The connectron that has the identifier 53537 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.781 KB and 4836.821 KB with a length of 0.041 KB. (4) The connectron that has the identifier 53541 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.877 KB and 4836.918 KB with a length of 0.042 KB. (5) The connectron that has the identifier 53544 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.940 KB and 4836.982 KB with a length of

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0.043 KB. (6) The connectron that has the identifier 53545 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.990 KB and 4837.123 KB with a length of 0.134 KB. (7) The connectron that has the

5   identifier 53548 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.126 KB and 4837.148 KB with a length of 0.023 KB. (8) The connectron that has the identifier 53551 is on chromosome 1 in the positive direction. The genomic start and stop positions of

10   this connectron are 4837.419 KB and 4837.448 KB with a length of 0.030 KB. (9) The connectron that has the identifier 53552 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.572 KB and 4837.622 KB with a length of 0.051 KB. (10) The connectron that has the

15   identifier 53554 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.962 KB and 4837.999 KB with a length of 0.038 KB. (11) The connectron that has the identifier 53557 is on chromosome 1 in the positive direction. The genomic start and stop positions of

20   this connectron are 4838.217 KB and 4838.258 KB with a length of 0.042 KB. (12) The connectron that has the identifier 53559 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.295 KB and 4838.362 KB with a length of 0.068 KB. (13) The connectron that has the

25   identifier 53563 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.457 KB and 4838.476 KB with a length of 0.020 KB. (14) The connectron that has the identifier 53564 is on chromosome 1 in the positive direction. The genomic start and stop positions of

30   this connectron are 4838.478 KB and 4838.645 KB with a length of 0.168 KB. (15) The connectron that has the identifier 53567 is on chromosome 1 in the positive direction. The genomic start and

stop positions of this connectron are 4838.654 KB and 4838.847
KB with a length of 0.194 KB.

Synthetic Connectron formed by a DBP

A synthetic connectron can be introduced into the *V. cholerae*
genome by introducing a 12-domain zinc-finger protein that
recognizes the sequence

tccccatgag catagatatg caggtaggcg gcaagt

Connectron 7580 is an example of a synthetic transient
connectron.

Global_Id	Chromosome	C1/C2		Chromosome	T1-T2		Connectron_Type
		C1_Id	C2_Id		T1_Id	T2_Id	
7580	1	Synthetic	DBP	1	607	646	synthetic

The T1-T2 target of the transient connectron 7580 as shown in
Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	607	1	1	952.642	952.777	.136		*-++++*+++*+++++++*+*++++*+*++++
TP	608	1	1	952.648	952.777	.130		*-++++-+++-*+++*+*-++*++++-++++
GG	609	1	1	952.846	954.393	1.548	Group0127	|||| ||| ||| | || |||| ||||
TN	610	1	1	954.486	954.587	.102		*-++++*+++*-+++-+-*+*-++*+**+++
TP	611	1	1	954.486	954.587	.102		*-+++++++++**++*+*++-**+-++-+*+
CNT	612	1	1	954.497	954.589	.093	OS->	|||||||||| ||||||| | | || | |
CPT	613	1	1	954.503	954.520	.018	-->	|||||||||| ||||||| | | || | |
CPT	614	1	1	954.522	954.588	.067	-->	|||||||||| ||||||| | | || | |
TP	615	1	1	954.601	954.658	.058		*-++++++++++*+++++++*+*+*++-+-*
TN	616	1	1	954.602	954.658	.057		*-+++++++++++++++++*+++++*+***-
CNT	617	1	1	954.616	954.658	.043	-->	|||||||||||||||| ||||| || |
CPT	618	1	1	954.624	954.639	.016	-->	|||||||||||||||| ||||| || |
CPT	619	1	1	954.641	954.658	.018	-->	|||||||||||||||| ||||| || |

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      GG    620   1 1   954.684   958.635    3.951 Group0128  |||||||||||||||||| ||||| || |
      GP    621   1 1   955.956   956.342     .387 VC0897     |||||||||||||||||| ||||| || |
      CPT   622   1 1   956.873   956.887     .015      -->   |||||||||||||||||| ||||| || |
      CPT   623   1 1   956.896   956.910     .015      -->   |||||||||||||||||| ||||| || |
   5  TN    624   1 1   958.089   958.103     .015      *-+*|||||||||||||||| ||||| || |
      GG    625   1 1   958.840   972.992   14.152 Group0129  | ||||||||||||||||| ||||| || |
      GP    626   1 1   971.304   972.992    1.689 VC0911     | ||||||||||||||||| ||||| || |
      TP    627   1 1   973.170   973.250     .081      *-+*|||||||||||||||| ||||| || |
      GG    628   1 1   973.171   973.763     .592 Group0130  |||||||||||||||||| ||||| || |
  10  CPT   629   1 1   973.339   973.434     .096      OS->  |||||||||||||||||| ||||| || |
      CPT   630   1 1   973.508   973.603     .096      OS->  |||||||||||||||||| ||||| || |
      TP    631  . 1 1   973.693   973.773     .081      *-+*|||||||||||||||| ||||| || |
      GG    632   1 1   973.767   996.501   22.734 Group0131  | ||||||||||||||||| ||||| || |
      GP    633   1 1   974.049   978.217    4.169 VC0913     | ||||||||||||||||| ||||| || |
  15  CPT   634   1 1   977.711   977.725     .015      -->   | ||||||||||||||||| ||||| || |
      CPT   635   1 1   977.732   977.746     .015      -->   | ||||||||||||||||| ||||| || |
      GP    636   1 1   986.166   990.921    4.756 VC0923     | ||||||||||||||||| ||||| || |
      CPT   637   1 1   986.862   986.877     .016      -->   | ||||||||||||||||| ||||| || |
      CPT   638   1 1   986.885   986.899     .015      -->   | ||||||||||||||||| ||||| || |
  20  TN    639   1 1   996.556   996.577     .022      *-+**|||||||||||||||| ||||| || |
      TP    640   1 1   996.556   996.577     .022      *-++-+++*++++++++++*||||| || |
      GG    641   1 1   996.656  1005.792    9.136 Group0132  || ||| |||||||||||||||| || |
      GP    642   1 1  1002.462  1005.792    3.331 VC0937     || ||| |||||||||||||||| || |
      TP    643   1 1  1005.810  1005.874     .065      *-++*+++*++*+*++++++++++*++*+*
  25  CNT   644   1 1  1005.810  1005.921     .112      OS->  ||||||||| | |||||||||||||||||
      CPT   645   1 1  1005.810  1005.926     .117      -->   ||||||||| | |||||||||||||||||
      TN    646   1 1  1005.810  1005.926     .117      *-++++*+++++*+*++++++++*+++*+++
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Group0127 through Group0132 are described in Table 2 as

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--------------------------------------------------------------------
Group0127


Gene_Name  COG_Id      Chromosome Direction    Start      Stop      Length
VC0894     COG0607     P          1 positive   952.846    954.393    1.548
--------------------------------------------------------------------
Group0128


Gene_Name  COG_Id      Chromosome Direction    Start      Stop      Length
VC0895                            1 negative   954.684    954.860     .177
VC0896     COG0583     K          1 positive   955.014    955.934     .921
VC0897     COG2363     S          1 positive   955.956    956.342     .387
VC0898     COG0258     L          1 negative   956.372    957.223     .852
VC0899     COG1611     R          1 negative   957.262    958.635    1.374
--------------------------------------------------------------------
Group0129
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Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0900	COG2199	T	1	negative	958.840	960.414	1.575
VC0901	COG0457	R	1	negative	960.516	962.777	2.262
VC0902	COG0780	R	1	negative	962.792	963.655	.864
VC0903			1	positive	963.686	964.282	.597
VC0904			1	positive	964.284	965.060	.777
VC0905	COG1464	M	1	negative	965.193	966.020	.828
VC0906	COG2011	R	1	negative	966.039	967.740	1.702
VC0908	COG0241	E	1	positive	967.976	968.536	.561
VC0909	COG1609	K	1	positive	968.601	969.551	.951
VC0910	COG1263	G	1	positive	969.788	971.224	1.437
VC0911	COG0366	G	1	positive	971.304	972.992	1.689

Group0130

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Tyr-2		1	positive	973.171	973.255	.085
tRNA-Tyr-3		1	positive	973.340	973.424	.085
tRNA-Tyr-4		1	positive	973.509	973.593	.085
tRNA-Tyr-5		1	positive	973.679	973.763	.085

Group0131

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0912			1	positive	973.767	973.862	.096
VC0913	COG0845	Q	1	positive	974.049	978.217	4.169
VC0915			1	positive	978.272	978.382	.111
VC0916	COG0394	T	1	positive	978.644	979.144	.501
VC0917	COG0381	M	1	positive	979.457	980.575	1.119
VC0918	COG0677	M	1	positive	980.595	986.155	5.561
VC0923	COG1045	E	1	positive	986.166	990.921	4.756
VC0928			1	positive	991.117	991.932	.816
VC0929			1	negative	992.138	993.364	1.227
VC0930			1	positive	993.628	996.501	2.874

Group0132

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
VC0931	COG3307	M	1	negative	996.656	997.972	1.317
VC0932			1	negative	998.148	998.752	.605
VC0934	COG2148	M	1	positive	999.242	1000.639	1.398
VC0935			1	positive	1000.710	1001.906	1.197
VC0936	COG1596	M	1	positive	1001.910	1002.437	.528
VC0937	COG3206	N	1	positive	1002.462	1005.792	3.331

All of the data for the transient connectron 7580 are pulled together in the following table that is the "terse" description of the connectron.

5   ---

Connectron Relationships - Global_Id   Type
                          7580   synthetic

10   Control Sequences - Synthetic DNA Binding Protein that recognizes the sequence
     tccccatgag catagatatg caggtaggcg gcaagt

Target Sequences - Direction Chromosome   T1_Id   Start   Stop Length
                    negative   1   607   952.777   952.642   .136
15

                                            T2_Id   Start   Stop Length
                                              646   1005.926 1005.810   .117

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816

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27	1	Group0131	VC0929		negative	993.364	992.138	1.227
28	1	Group0131	VC0930		positive	993.628	996.501	2.874
29	1	Group0132	VC0931	COG3307	positive	996.656	1005.792	9.136
30	1	Group0132	VC0932		negative	998.752	998.148	.605
31	1	Group0132	VC0934	COG2148	positive	999.242	1000.639	1.398
32	1	Group0132	VC0935		positive	1000.710	1001.906	1.197
33	1	Group0132	VC0936	COG1596	positive	1001.910	1002.437	.528
34	1	Group0132	VC0937	COG3206	positive	1002.462	1005.792	3.331

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	612	negative	954.589	954.497	.093
2	1	613	positive	954.503	954.520	.018
3	1	614	positive	954.522	954.588	.067
4	1	617	negative	954.658	954.616	.043
5	1	618	positive	954.624	954.639	.016
6	1	619	positive	954.641	954.658	.018
7	1	622	positive	956.873	956.887	.015
8	1	623	positive	956.896	956.910	.015
9	1	629	positive	973.339	973.434	.096
10	1	630	positive	973.508	973.603	.096
11	1	634	positive	977.711	977.725	.015
12	1	635	positive	977.732	977.746	.015
13	1	637	positive	986.862	986.877	.016
14	1	638	positive	986.885	986.899	.015
15	1	644	negative	1005.921	1005.810	.112
16	1	645	positive	1005.810	1005.926	.117

The verbose description of the synthetic connectron 7580 is:

In the Vibrio cholerae chromosome I, complete chromosome the synthetic connectron number 7580 is generated by a synthetic DNA binding protein that recognizes the sequence tccccatgagcatagatatgcaggtaggcggcaagt. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is 607. The genomic start and stop positions of this initiating target sequence are 952.777 KB and 952.642 KB with a length of 0.136 KB. The identifier number of the terminating target

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sequence (T2) is 646. The genomic start and stop positions of this terminating target sequence are 1005.926 KB and 1005.810 KB with a length of 0.117 KB.

5   This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name VC0894 and with a COG identifier of COG0607. The genomic start and stop positions of this gene are 952.846 KB and 954.393 KB with a length of 1.548 KB. (2) The gene that has the name VC0895. The

10   genomic start and stop positions of this gene are 954.684 KB and 958.635 KB with a length of 3.951 KB. (3) The gene that has the name VC0896 and with a COG identifier of COG0583. The genomic start and stop positions of this gene are 955.014 KB and 955.934 KB with a length of 0.921 KB. (4) The gene that has the name

15   VC0897 and with a COG identifier of COG2363. The genomic start and stop positions of this gene are 955.956 KB and 956.342 KB with a length of 0.387 KB. (5) The gene that has the name VC0898 and with a COG identifier of COG0258. The genomic start and stop positions of this gene are 957.223 KB and 956.372 KB with a

20   length of 0.852 KB. (6) The gene that has the name VC0899 and with a COG identifier of COG1611. The genomic start and stop positions of this gene are 958.635 KB and 957.262 KB with a length of 1.374 KB. (7) The gene that has the name VC0900 and with a COG identifier of COG2199. The genomic start and stop

25   positions of this gene are 958.840 KB and 972.992 KB with a length of 14.152 KB. (8) The gene that has the name VC0901 and with a COG identifier of COG0457. The genomic start and stop positions of this gene are 962.777 KB and 960.516 KB with a length of 2.262 KB. (9) The gene that has the name VC0902 and

30   with a COG identifier of COG0780. The genomic start and stop positions of this gene are 963.655 KB and 962.792 KB with a length of 0.864 KB. (10) The gene that has the name VC0903. The

genomic start and stop positions of this gene are 963.686 KB and 964.282 KB with a length of 0.597 KB. (11) The gene that has the name VC0904. The genomic start and stop positions of this gene are 964.284 KB and 965.060 KB with a length of 0.777 KB. (12) The gene that has the name VC0905 and with a COG identifier of COG1464. The genomic start and stop positions of this gene are 966.020 KB and 965.193 KB with a length of 0.828 KB. (13) The gene that has the name VC0906 and with a COG identifier of COG2011. The genomic start and stop positions of this gene are 967.740 KB and 966.039 KB with a length of 1.702 KB. (14) The gene that has the name VC0908 and with a COG identifier of COG0241. The genomic start and stop positions of this gene are 967.976 KB and 968.536 KB with a length of 0.561 KB. (15) The gene that has the name VC0909 and with a COG identifier of COG1609. The genomic start and stop positions of this gene are 968.601 KB and 969.551 KB with a length of 0.951 KB. (16) The gene that has the name VC0910 and with a COG identifier of COG1263. The genomic start and stop positions of this gene are 969.788 KB and 971.224 KB with a length of 1.437 KB. (17) The gene that has the name VC0911 and with a COG identifier of COG0366. The genomic start and stop positions of this gene are 971.304 KB and 972.992 KB with a length of 1.689 KB. (18) The gene that has the name tRNA-Tyr-. The genomic start and stop positions of this gene are 973.171 KB and 973.763 KB with a length of 0.592 KB. (19) The gene that has the name VC0912. The genomic start and stop positions of this gene are 973.767 KB and 996.501 KB with a length of 22.734 KB. (20) The gene that has the name VC0913 and with a COG identifier of COG0845. The genomic start and stop positions of this gene are 974.049 KB and 978.217 KB with a length of 4.169 KB. (21) The gene that has the name VC0915. The genomic start and stop positions of this gene are 978.272 KB and 978.382 KB with a length of 0.111 KB. (22)

The gene that has the name VC0916 and with a COG identifier of COG0394. The genomic start and stop positions of this gene are 978.644 KB and 979.144 KB with a length of 0.501 KB. (23) The gene that has the name VC0917 and with a COG identifier of

5   COG0381. The genomic start and stop positions of this gene are 979.457 KB and 980.575 KB with a length of 1.119 KB. (24) The gene that has the name VC0918 and with a COG identifier of COG0677. The genomic start and stop positions of this gene are 980.595 KB and 986.155 KB with a length of 5.561 KB. (25) The

10   gene that has the name VC0923 and with a COG identifier of COG1045. The genomic start and stop positions of this gene are 986.166 KB and 990.921 KB with a length of 4.756 KB. (26) The gene that has the name VC0928. The genomic start and stop positions of this gene are 991.117 KB and 991.932 KB with a

15   length of 0.816 KB. (27) The gene that has the name VC0929. The genomic start and stop positions of this gene are 993.364 KB and 992.138 KB with a length of 1.227 KB. (28) The gene that has the name VC0930. The genomic start and stop positions of this gene are 993.628 KB and 996.501 KB with a length of 2.874 KB. (29)

20   The gene that has the name VC0931 and with a COG identifier of COG3307. The genomic start and stop positions of this gene are 996.656 KB and 1005.792 KB with a length of 9.136 KB. (30) The gene that has the name VC0932. The genomic start and stop positions of this gene are 998.752 KB and 998.148 KB with a

25   length of 0.605 KB. (31) The gene that has the name VC0934 and with a COG identifier of COG2148. The genomic start and stop positions of this gene are 999.242 KB and 1000.639 KB with a length of 1.398 KB. (32) The gene that has the name VC0935. The genomic start and stop positions of this gene are 1000.710 KB

30   and 1001.906 KB with a length of 1.197 KB. (33) The gene that has the name VC0936 and with a COG identifier of COG1596. The genomic start and stop positions of this gene are 1001.910 KB

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and 1002.437 KB with a length of 0.528 KB. (34) The gene that
has the name VC0937 and with a COG identifier of COG3206. The
genomic start and stop positions of this gene are 1002.462 KB
and 1005.792 KB with a length of 3.331 KB.

5

This connectron controls the turning off of the expression of
the following connectron(s): (1) The connectron that has the
identifier 612 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 954.589
10 KB and 954.497 KB with a length of 0.093 KB. (2) The connectron
that has the identifier 613 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this
connectron are 954.503 KB and 954.520 KB with a length of 0.018
KB. (3) The connectron that has the identifier 614 is on
15 chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 954.522 KB and 954.588 KB
with a length of 0.067 KB. (4) The connectron that has the
identifier 617 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 954.658
20 KB and 954.616 KB with a length of 0.043 KB. (5) The connectron
that has the identifier 618 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this
connectron are 954.624 KB and 954.639 KB with a length of 0.016
KB. (6) The connectron that has the identifier 619 is on
25 chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 954.641 KB and 954.658 KB
with a length of 0.018 KB. (7) The connectron that has the
identifier 622 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 956.873
30 KB and 956.887 KB with a length of 0.015 KB. (8) The connectron
that has the identifier 623 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this

connectron are 956.896 KB and 956.910 KB with a length of 0.015 KB. (9) The connectron that has the identifier 629 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.339 KB and 973.434 KB with a length of 0.096 KB. (10) The connectron that has the identifier 630 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.508 KB and 973.603 KB with a length of 0.096 KB. (11) The connectron that has the identifier 634 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 977.711 KB and 977.725 KB with a length of 0.015 KB. (12) The connectron that has the identifier 635 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 977.732 KB and 977.746 KB with a length of 0.015 KB. (13) The connectron that has the identifier 637 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.862 KB and 986.877 KB with a length of 0.016 KB. (14) The connectron that has the identifier 638 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.885 KB and 986.899 KB with a length of 0.015 KB. (15) The connectron that has the identifier 644 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 1005.921 KB and 1005.810 KB with a length of 0.112 KB. (16) The connectron that has the identifier 645 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 1005.810 KB and 1005.926 KB with a length of 0.117 KB.

Synthetic Connectron formed by a PNA

A synthetic connectron can be introduced into the *V. cholerae*
genome by introducing a PNA that recognizes the sequence

5   tccccatgag catagatatg caggtaggcg gcaagt

Connectron 7581 is an example of a synthetic transient
connectron.

10   C1/C2   T1-T2
      Global_Id Chromosome C1_Id   C2_Id Chromosome T1_Id   T2_Id   Connectron_Type
          7581   1   Synthetic PNA   1   607   646   synthetic

The T1-T2 target of the transient connectron 7581 as shown in
15 Table 1 is represented as

```
      Type   Num Jobno  Chr   Start     Stop    Length GeneName
      TN     607   1   1   952.642   952.777    .136              *-++++*+++*++++++*+*++++**++++
      TP     608   1   1   952.648   952.777    .130              *-++++-+++-*+++*+*-++*++++-++++
20    GG     609   1   1   952.846   954.393   1.548 Group0127    ||||  |||   ||| |  || |||| ||||
      TN     610   1   1   954.486   954.587    .102              *-++++*+++-++-+-*+*-++*+*+++
      TP     611   1   1   954.486   954.587    .102              *-+++++++++*+*++*+*++-**+-++-+*+
      CNT    612   1   1   954.497   954.589    .093      OS->  |||||||||| ||||||| | | || | |
      CPT    613   1   1   954.503   954.520    .018      -->   |||||||||| ||||||| | | || | |
25    CPT    614   1   1   954.522   954.588    .067      -->   |||||||||| ||||||| | | || | |
      TP     615   1   1   954.601   954.658    .058              *-++++++++++*++++++*+*+*++-+-*
      TN     616   1   1   954.602   954.658    .057              *-++++++++++++++++++*+++++*+**-
      CNT    617   1   1   954.616   954.658    .043      -->   ||||||||||||||||| ||||| || |
      CPT    618   1   1   954.624   954.639    .016      -->   ||||||||||||||||| ||||| || |
30    CPT    619   1   1   954.641   954.658    .018      -->   ||||||||||||||||| ||||| || |
      GG     620   1   1   954.684   958.635   3.951 Group0128  ||||||||||||||||| ||||| || |
      GP     621   1   1   955.956   956.342    .387 VC0897     ||||||||||||||||| ||||| || |
      CPT    622   1   1   956.873   956.887    .015      -->   ||||||||||||||||| ||||| || |
      CPT    623   1   1   956.896   956.910    .015      -->   ||||||||||||||||| ||||| || |
35    TN     624   1   1   958.089   958.103    .015              *-+*||||||||||||||| ||||| || |
      GG     625   1   1   958.840   972.992  14.152 Group0129  | ||||||||||||||||| ||||| || |
      GP     626   1   1   971.304   972.992   1.689 VC0911     | ||||||||||||||| ||||| || |
      TP     627   1   1   973.170   973.250    .081              *-+*||||||||||||||| ||||| || |
      GG     628   1   1   973.171   973.763    .592 Group0130  ||||||||||||||||| ||||| || |
40    CPT    629   1   1   973.339   973.434    .096      OS->  ||||||||||||||||| ||||| || |
      CPT    630   1   1   973.508   973.603    .096      OS->  ||||||||||||||||| ||||| || |
      TP     631   1   1   973.693   973.773    .081              *-+*||||||||||||||| ||||| || |
```

```
        GG      632   1  1    973.767    996.501   22.734 Group0131   | |||||||||||||||| ||||| || |
        GP      633   1  1    974.049    978.217    4.169 VC0913      | |||||||||||||||| ||||| || |
        CPT     634   1  1    977.711    977.725     .015     -->     | |||||||||||||||| ||||| || |
        CPT     635   1  1    977.732    977.746     .015     -->     | |||||||||||||||| ||||| || |
  5     GP      636   1  1    986.166    990.921    4.756 VC0923      | |||||||||||||||| ||||| || |
        CPT     637   1  1    986.862    986.877     .016     -->     | |||||||||||||||| ||||| || |
        CPT     638   1  1    986.885    986.899     .015     -->     | |||||||||||||||| ||||| || |
        TN      639   1  1    996.556    996.577     .022             *-+**|||||||||||||| ||||| || |
        TP      640   1  1    996.556    996.577     .022             *-++-+++*+++++++++*||||| || |
 10     GG      641   1  1    996.656   1005.792    9.136 Group0132   || ||| |||||||||||||||| || |
        GP      642   1  1   1002.462   1005.792    3.331 VC0937      || ||| |||||||||||||||| || |
        TP      643   1  1   1005.810   1005.874     .065             *-++*+++*++*+*+++++++++*++*+*
        CNT     644   1  1   1005.810   1005.921     .112     OS->    ||||||||| | |||||||||||||||||
        CPT     645   1  1   1005.810   1005.926     .117     -->     ||||||||| | |||||||||||||||||
 15     TN      646   1  1   1005.810   1005.926     .117             *-++++*++++*+*+++++++++*+++*+++
```

Group0127 through Group0132 are described in Table 2 as

```
         ----------------------------------------------------------------
 20      Group0127

         Gene_Name   COG_Id        Chromosome  Direction    Start      Stop      Length
         VC0894      COG0607    P           1   positive   952.846   954.393      1.548
         ----------------------------------------------------------------
 25      Group0128

         Gene_Name   COG_Id        Chromosome  Direction    Start      Stop      Length
         VC0895                              1   negative   954.684   954.860       .177
         VC0896      COG0583    K           1   positive   955.014   955.934       .921
 30      VC0897      COG2363    S           1   positive   955.956   956.342       .387
         VC0898      COG0258    L           1   negative   956.372   957.223       .852
         VC0899      COG1611    R           1   negative   957.262   958.635      1.374

         ----------------------------------------------------------------
         Group0129
 35
         Gene_Name   COG_Id        Chromosome  Direction    Start      Stop      Length
         VC0900      COG2199    T           1   negative   958.840   960.414      1.575
         VC0901      COG0457    R           1   negative   960.516   962.777      2.262
         VC0902      COG0780    R           1   negative   962.792   963.655       .864
 40      VC0903                             1   positive   963.686   964.282       .597
         VC0904                             1   positive   964.284   965.060       .777
         VC0905      COG1464    M           1   negative   965.193   966.020       .828
         VC0906      COG2011    R           1   negative   966.039   967.740      1.702
         VC0908      COG0241    E           1   positive   967.976   968.536       .561
 45      VC0909      COG1609    K           1   positive   968.601   969.551       .951
         VC0910      COG1263    G           1   positive   969.788   971.224      1.437
         VC0911      COG0366    G           1   positive   971.304   972.992      1.689
```

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```
------------------------------------------------------------------
Group0130

Gene_Name  COG_Id      Chromosome  Direction   Start      Stop    Length
tRNA-Tyr-2                       1  positive  973.171   973.255     .085
tRNA-Tyr-3                       1  positive  973.340   973.424     .085
tRNA-Tyr-4                       1  positive  973.509   973.593     .085
tRNA-Tyr-5                       1  positive  973.679   973.763     .085
------------------------------------------------------------------
Group0131

Gene_Name  COG_Id      Chromosome  Direction   Start      Stop    Length
VC0912                           1  positive  973.767   973.862     .096
VC0913     COG0845  Q            1  positive  974.049   978.217    4.169
VC0915                           1  positive  978.272   978.382     .111
VC0916     COG0394  T            1  positive  978.644   979.144     .501
VC0917     COG0381  M            1  positive  979.457   980.575    1.119
VC0918     COG0677  M            1  positive  980.595   986.155    5.561
VC0923     COG1045  E            1  positive  986.166   990.921    4.756
VC0928                           1  positive  991.117   991.932     .816
VC0929                           1  negative  992.138   993.364    1.227
VC0930                           1  positive  993.628   996.501    2.874
------------------------------------------------------------------
Group0132

Gene_Name  COG_Id      Chromosome  Direction    Start      Stop    Length
VC0931     COG3307  M            1  negative   996.656   997.972    1.317
VC0932                           1  negative   998.148   998.752     .605
VC0934     COG2148  M            1  positive   999.242  1000.639    1.398
VC0935                           1  positive  1000.710  1001.906    1.197
VC0936     COG1596  M            1  positive  1001.910  1002.437     .528
VC0937     COG3206  N            1  positive  1002.462  1005.792    3.331
------------------------------------------------------------------
```

All of the data for the transient connectron 7581 are pulled together in the following table that is the "terse" description of the connectron.

```
------------------------------------------------------------------

Connectron Relationships - Global_Id  Type
                                7581  synthetic

Control Sequences - Synthetic PNA that recognizes the sequence
tccccatgag  catagatatg  caggtaggcg  gcaagt
```

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```
Target Sequences  - Direction  Chromosome      T1_Id     Start      Stop  Length
                    negative             1        607   952.777   952.642    .136


                                                 T2_Id     Start      Stop  Length
                                                   646  1005.926  1005.810    .117
```

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816
27	1	Group0131	VC0929		negative	993.364	992.138	1.227
28	1	Group0131	VC0930		positive	993.628	996.501	2.874
29	1	Group0132	VC0931	COG3307	positive	996.656	1005.792	9.136
30	1	Group0132	VC0932		negative	998.752	998.148	.605
31	1	Group0132	VC0934	COG2148	positive	999.242	1000.639	1.398
32	1	Group0132	VC0935		positive	1000.710	1001.906	1.197
33	1	Group0132	VC0936	COG1596	positive	1001.910	1002.437	.528
34	1	Group0132	VC0937	COG3206	positive	1002.462	1005.792	3.331

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	612	negative	954.589	954.497	.093
2	1	613	positive	954.503	954.520	.018
3	1	614	positive	954.522	954.588	.067

4	1	617	negative	954.658	954.616	.043
5	1	618	positive	954.624	954.639	.016
6	1	619	positive	954.641	954.658	.018
7	1	622	positive	956.873	956.887	.015
8	1	623	positive	956.896	956.910	.015
9	1	629	positive	973.339	973.434	.096
10	1	630	positive	973.508	973.603	.096
11	1	634	positive	977.711	977.725	.015
12	1	635	positive	977.732	977.746	.015
13	1	637	positive	986.862	986.877	.016
14	1	638	positive	986.885	986.899	.015
15	1	644	negative	1005.921	1005.810	.112
16	1	645	positive	1005.810	1005.926	.117

The verbose description of the synthetic connectron 7581 is:

In the Vibrio cholerae chromosome I, complete chromosome the
synthetic connectron number 7580 is generated by a synthetic PNA
that recognizes the sequence
tccccatgagcatagatatgcaggtaggcggcaagt. This connectron causes
stabilization of a loop of DNA. The target sequences (T1-T2)
are on the negative strand of the genomic DNA on chromosome 1.
The identifier number of the initiating target sequence (T1) is
607. The genomic start and stop positions of this initiating
target sequence are 952.777 KB and 952.642 KB with a length of
0.136 KB. The identifier number of the terminating target
sequence (T2) is 646. The genomic start and stop positions of
this terminating target sequence are 1005.926 KB and 1005.810 KB
with a length of 0.117 KB.

This connectron controls the modulation of the expression of the
following gene(s): (1) The gene that has the name VC0894 and
with a COG identifier of COG0607. The genomic start and stop
positions of this gene are 952.846 KB and 954.393 KB with a
length of 1.548 KB. (2) The gene that has the name VC0895. The

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genomic start and stop positions of this gene are 954.684 KB and 958.635 KB with a length of 3.951 KB. (3) The gene that has the name VC0896 and with a COG identifier of COG0583. The genomic start and stop positions of this gene are 955.014 KB and 955.934 KB with a length of 0.921 KB. (4) The gene that has the name VC0897 and with a COG identifier of COG2363. The genomic start and stop positions of this gene are 955.956 KB and 956.342 KB with a length of 0.387 KB. (5) The gene that has the name VC0898 and with a COG identifier of COG0258. The genomic start and stop positions of this gene are 957.223 KB and 956.372 KB with a length of 0.852 KB. (6) The gene that has the name VC0899 and with a COG identifier of COG1611. The genomic start and stop positions of this gene are 958.635 KB and 957.262 KB with a length of 1.374 KB. (7) The gene that has the name VC0900 and with a COG identifier of COG2199. The genomic start and stop positions of this gene are 958.840 KB and 972.992 KB with a length of 14.152 KB. (8) The gene that has the name VC0901 and with a COG identifier of COG0457. The genomic start and stop positions of this gene are 962.777 KB and 960.516 KB with a length of 2.262 KB. (9) The gene that has the name VC0902 and with a COG identifier of COG0780. The genomic start and stop positions of this gene are 963.655 KB and 962.792 KB with a length of 0.864 KB. (10) The gene that has the name VC0903. The genomic start and stop positions of this gene are 963.686 KB and 964.282 KB with a length of 0.597 KB. (11) The gene that has the name VC0904. The genomic start and stop positions of this gene are 964.284 KB and 965.060 KB with a length of 0.777 KB. (12) The gene that has the name VC0905 and with a COG identifier of COG1464. The genomic start and stop positions of this gene are 966.020 KB and 965.193 KB with a length of 0.828 KB. (13) The gene that has the name VC0906 and with a COG identifier of COG2011. The genomic start and stop positions of this gene are

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967.740 KB and 966.039 KB with a length of 1.702 KB. (14) The gene that has the name VC0908 and with a COG identifier of COG0241. The genomic start and stop positions of this gene are 967.976 KB and 968.536 KB with a length of 0.561 KB. (15) The gene that has the name VC0909 and with a COG identifier of COG1609. The genomic start and stop positions of this gene are 968.601 KB and 969.551 KB with a length of 0.951 KB. (16) The gene that has the name VC0910 and with a COG identifier of COG1263. The genomic start and stop positions of this gene are 969.788 KB and 971.224 KB with a length of 1.437 KB. (17) The gene that has the name VC0911 and with a COG identifier of COG0366. The genomic start and stop positions of this gene are 971.304 KB and 972.992 KB with a length of 1.689 KB. (18) The gene that has the name tRNA-Tyr-. The genomic start and stop positions of this gene are 973.171 KB and 973.763 KB with a length of 0.592 KB. (19) The gene that has the name VC0912. The genomic start and stop positions of this gene are 973.767 KB and 996.501 KB with a length of 22.734 KB. (20) The gene that has the name VC0913 and with a COG identifier of COG0845. The genomic start and stop positions of this gene are 974.049 KB and 978.217 KB with a length of 4.169 KB. (21) The gene that has the name VC0915. The genomic start and stop positions of this gene are 978.272 KB and 978.382 KB with a length of 0.111 KB. (22) The gene that has the name VC0916 and with a COG identifier of COG0394. The genomic start and stop positions of this gene are 978.644 KB and 979.144 KB with a length of 0.501 KB. (23) The gene that has the name VC0917 and with a COG identifier of COG0381. The genomic start and stop positions of this gene are 979.457 KB and 980.575 KB with a length of 1.119 KB. (24) The gene that has the name VC0918 and with a COG identifier of COG0677. The genomic start and stop positions of this gene are 980.595 KB and 986.155 KB with a length of 5.561 KB. (25) The

gene that has the name VC0923 and with a COG identifier of COG1045. The genomic start and stop positions of this gene are 986.166 KB and 990.921 KB with a length of 4.756 KB. (26) The gene that has the name VC0928. The genomic start and stop positions of this gene are 991.117 KB and 991.932 KB with a length of 0.816 KB. (27) The gene that has the name VC0929. The genomic start and stop positions of this gene are 993.364 KB and 992.138 KB with a length of 1.227 KB. (28) The gene that has the name VC0930. The genomic start and stop positions of this gene are 993.628 KB and 996.501 KB with a length of 2.874 KB. (29) The gene that has the name VC0931 and with a COG identifier of COG3307. The genomic start and stop positions of this gene are 996.656 KB and 1005.792 KB with a length of 9.136 KB. (30) The gene that has the name VC0932. The genomic start and stop positions of this gene are 998.752 KB and 998.148 KB with a COG identifier of COG2148. The genomic start and stop positions of this gene are 999.242 KB and 1000.639 KB with a length of 1.398 KB. (32) The gene that has the name VC0935. The genomic start and stop positions of this gene are 1000.710 KB and 1001.906 KB with a length of 1.197 KB. (33) The gene that has the name VC0936 and with a COG identifier of COG1596. The genomic start and stop positions of this gene are 1001.910 KB and 1002.437 KB with a length of 0.528 KB. (34) The gene that has the name VC0937 and with a COG identifier of COG3206. The genomic start and stop positions of this gene are 1002.462 KB and 1005.792 KB with a length of 3.331 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 612 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 954.589

KB and 954.497 KB with a length of 0.093 KB. (2) The connectron that has the identifier 613 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.503 KB and 954.520 KB with a length of 0.018

5   KB. (3) The connectron that has the identifier 614 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.522 KB and 954.588 KB with a length of 0.067 KB. (4) The connectron that has the identifier 617 is on chromosome 1 in the negative direction. The

10   genomic start and stop positions of this connectron are 954.658 KB and 954.616 KB with a length of 0.043 KB. (5) The connectron that has the identifier 618 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.624 KB and 954.639 KB with a length of 0.016

15   KB. (6) The connectron that has the identifier 619 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.641 KB and 954.658 KB with a length of 0.018 KB. (7) The connectron that has the identifier 622 is on chromosome 1 in the positive direction. The

20   genomic start and stop positions of this connectron are 956.873 KB and 956.887 KB with a length of 0.015 KB. (8) The connectron that has the identifier 623 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 956.896 KB and 956.910 KB with a length of 0.015

25   KB. (9) The connectron that has the identifier 629 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.339 KB and 973.434 KB with a length of 0.096 KB. (10) The connectron that has the identifier 630 is on chromosome 1 in the positive direction. The

30   genomic start and stop positions of this connectron are 973.508 KB and 973.603 KB with a length of 0.096 KB. (11) The connectron that has the identifier 634 is on chromosome 1 in the positive

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direction. The genomic start and stop positions of this
connectron are 977.711 KB and 977.725 KB with a length of 0.015
KB. (12) The connectron that has the identifier 635 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 977.732 KB and 977.746 KB
with a length of 0.015 KB. (13) The connectron that has the
identifier 637 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 986.862
KB and 986.877 KB with a length of 0.016 KB. (14) The connectron
that has the identifier 638 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this
connectron are 986.885 KB and 986.899 KB with a length of 0.015
KB. (15) The connectron that has the identifier 644 is on
chromosome 1 in the negative direction. The genomic start and
stop positions of this connectron are 1005.921 KB and 1005.810
KB with a length of 0.112 KB. (16) The connectron that has the
identifier 645 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 1005.810
KB and 1005.926 KB with a length of 0.117 KB.

**Synthetic Connectron formed by a Pair of Linked DNA Binding
Objects**

A synthetic connectron can be introduced into the *A. pernix*
genome by introducing a pair of linked DNA binding objects that
recognize the sequences

G1   cccgacacaacctgc
and
G2   cccggggttcccgag

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Connectron 917 is an example of a synthetic transient connectron.

Global_Id	Chromosome	C1/C2		Chromosome	T1-T2		Connectron_Type
		C1_Id	C2_Id		T1_Id	T2_Id	
917	1	G1	G2	1	218	295	synthetic

The T1-T2 target of the transient connectron 917 as shown in Table 1 is represented as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	218	1	1	284.008	284.071	.064		*-+*+-++*|||| |||	
TP	219	1	1	284.008	284.071	.064		*-+++*|| |||| |||	
CPT	220	1	1	284.009	284.071	.063		--> |||||| |||| |||	
CNT	221	1	1	284.073	284.144	.072		--> |||||| |||| |||	
CPT	222	1	1	284.073	284.145	.073		--> |||||| |||| |||	
TP	223	1	1	284.073	284.160	.088		*-++++++*++++*|||	
TN	224	1	1	284.073	284.251	.179		*-++++++++++++++**+*
CNT	225	1	1	284.158	284.251	.094		--> |||||||||||||||||
CPT	226	1	1	284.158	284.251	.094		--> |||||||||||||||||
TP	227	1	1	284.162	284.251	.090		*-+++++++++++++++++**
CPT	228	1	1	284.253	284.280	.028		--> ||||||||||||||||||||
TN	229	1	1	284.253	284.305	.053		*-++++++++++++++++++*
TP	230	1	1	284.253	284.316	.064		*-++++++++++++++++++**
CPT	231	1	1	284.283	284.305	.023		--> ||||||||||||||||||||||
GG	232	1	1	284.391	287.510	3.120	Group0053	|||||||||||||||||||||||
TN	233	1	1	286.094	286.108	.015		*-++++++++++++++++++++*
GG	234	1	1	287.521	291.639	4.118	Group0054	||||||||||||||||||||||||
TP	235	1	1	288.611	288.625	.015		*-+++++*|||||||||||||||||
GG	236	1	1	291.643	295.139	3.496	Group0055	|||||| |||||||||||||||||||
TP	237	1	1	295.230	295.259	.030		*-++++++*||||||||||||||||||
GG	238	1	1	295.231	295.529	.298	Group0056	||||||||||||||||||||||||||
GP	239	1	1	295.342	295.518	.177	APES013	||||||||||||||||||||||||||
CPT	240	1	1	295.415	295.444	.030		--> ||||||||||||||||||||||
TP	241	1	1	295.417	295.444	.028		*-+++++++++*++++++++++++*
GG	242	1	1	295.572	296.676	1.104	Group0057	||||||||| ||||||||||||||
TN	243	1	1	296.080	296.095	.016		*-+++++++++*|||||||||||||
TN	244	1	1	296.913	296.927	.015		*-+++++++++++++++++++++++*
GG	245	1	1	297.071	298.857	1.786	Group0058	||||||||||||||||||||||||||
TP	246	1	1	298.617	298.631	.015		*-+++++++++++++++++++++++*
GG	247	1	1	298.856	305.941	7.085	Group0059	||||||||||||||||||||||||||||
CNT	248	1	1	300.742	300.757	.016		--> |||||||||||||||||||||||||
CNT	249	1	1	300.767	300.781	.015		--> |||||||||||||||||||||||||
GN	250	1	1	301.243	303.153	1.911	APE0428	|||||||||||||||||||||||||
TN	251	1	1	301.733	301.748	.016		*-++++++++++++*++++++++++++*

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      GP    252   1  1   305.005   305.611    .607 APE0434    |||||||||||| |||||||||||||||||
      CPT   253   1  1   305.334   305.348    .015        --> |||||||||||| |||||||||||||||||
      CPT   254   1  1   305.358   305.372    .015        --> |||||||||||| |||||||||||||||||
      CNT   255   1  1   305.552   305.566    .015        --> |||||||||||| |||||||||||||||||
  5   TN    256   1  1   305.562   305.576    .015            *-++++++++++++*|||||||||||||||||
      CNT   257   1  1   305.568   305.582    .015        --> |||||||||||||||||||||||||||||||
      GG    258   1  1   306.121   308.859   2.738 Group0060  |||||||||||||||||||||||||||||||||
      TP    259   1  1   307.532   307.547    .016            *-+++++++++++++++++++++++++++++++
      TN    260   1  1   307.814   307.828    .015            *-+++++++++++++++++++++++++++++++
 10   TN    261   1  1   308.559   308.573    .015            *-+++++++++++++++++++++++++++++++
      GG    262   1  1   308.989   312.190   3.201 Group0061  ||||||||||||||||||||||||||||||
      TN    263   1  1   311.735   311.750    .016            *-+++++++++++++++++++++++++++++++
      GG    264   1  1   312.215   313.258   1.043 Group0062  |||||||||||||||||||||||||||||
      TP    265   1  1   312.894   312.909    .016            *-+++++++++++++++++++++++++++++++
 15   GG    266   1  1   313.378   315.728   2.350 Group0063  ||||||||||||||||||||||||||||||
      TN    267   1  1   314.051   314.065    .015            *-+++++++++++++++++++++++++++++++
      TN    268   1  1   314.826   314.840    .015            *-+++++++++++++++++++++++++++++++
      TN    269   1  1   315.511   315.525    .015            *-+++++++++++++++++++++++++++++++
      TP    270   1  1   315.747   315.761    .015            *-+++++++++++++++++++++++++++++++
 20   GG    271   1  1   315.792   318.996   3.204 Group0064  |||||||||||||||||||||||||||||||||
      GP    272   1  1   317.638   318.996   1.359 APE0457    |||||||||||||||||||||||||||||||||
      CNT   273   1  1   317.668   317.682    .015        --> |||||||||||||||||||||||||||||||||
      TP    274   1  1   317.689   317.703    .015            *-+++++++++++++++++++++++++++++++
      CNT   275   1  1   317.690   317.704    .015        --> |||||||||||||||||||||||||||||||||
 25   GG    276   1  1   318.432   318.914    .483 Group0065  |||||||||||||||||||||||||||||||
      CPT   277   1  1   319.097   319.127    .031        --> |||||||||||||||||||||||||||||||
      TN    278   1  1   319.122   319.137    .016            *-+++++++++++++++++++++++++++++++
      GG    279   1  1   319.335   319.673    .339 Group0066  |||||||||||||||||||||||||||||||
      TN    280   1  1   319.515   319.529    .015            *-+++++++++++++++++++++++++++++++
 30   TP    281   1  1   319.572   319.586    .015            *-+++++++++++++++++++++++++++++++
      GG    282   1  1   319.733   324.526   4.793 Group0067  ||||||||||||||||||||||||||||||||
      CNT   283   1  1   320.484   320.513    .030        --> ||||||||||||||||||||||||||||||||
      GN    284   1  1   320.700   322.241   1.542 APE0462    ||||||||||||||||||||||||||||||||
      TN    285   1  1   323.674   323.688    .015            *-+++++++++*|||||||||||||||||||||
 35   GG    286   1  1   324.030   324.335    .306 Group0068  |||||||| |||||||||||||||||||||
      TN    287   1  1   324.137   324.151    .015            *-++++++++-++++++++++++++++++++
      GG    288   1  1   324.606   325.575    .969 Group0069  |||||||| |||||||||||||||||||||
      GP    289   1  1   325.141   325.575    .435 APE0469    |||||||| |||||||||||||||||||||
      CNT   290   1  1   325.950   325.979    .030        --> |||||||| |||||||||||||||||||||
 40   CPT   291   1  1   325.950   325.979    .030        --> |||||||| |||||||||||||||||||||
      TN    292   1  1   325.959   325.975    .017            *-++++++++-+*+++++++++++++++++++
      GG    293   1  1   325.980   326.717    .738 Group0070  |||||||| | |||||||||||||||||||
      CNT   294   1  1   326.716   326.878    .163      OS-> |||||||| | |||||||||||||||||||
      TN    295   1  1   326.716   326.878    .163            *-+*+++++*-+-++++*|||||||||||||
 45
```

The "Type" descriptor of the T1 (Id number 218) is "TN" showing
that is T1 target is on the negative strand of the double-

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stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 295) also has the type descriptor "TN".

5   Group0053 through Group0070 are described in Table 2 as

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Group0053
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10
Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0413	COG0553	K	1	negative	284.391	287.510	3.120

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------------------------------------------------------------------
Group0054
```

15
Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0414			1	negative	287.521	288.066	.546
APE0415	COG1483	R	1	negative	288.073	291.639	3.567

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Group0055
```

20
Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0416	COG1743	L	1	negative	291.643	294.666	3.024
APE0417			1	positive	292.319	292.636	.318
APE0418			1	positive	294.690	295.139	.450

25
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Group0056
```

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Thr		1	positive	295.231	295.325	.095
APES013		1	positive	295.342	295.518	.177
tRNA-Met		1	positive	295.405	295.529	.125

30

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Group0057
```

35
Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APES014		1	negative	295.572	295.754	.183
APE0419		1	negative	295.891	296.676	.786

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------------------------------------------------------------------
Group0058
```

40
Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0420			1	positive	297.071	298.113	1.043
APE0422			1	negative	297.448	297.993	.546
APE0423	COG0084	L	1	negative	298.099	298.857	.759

45
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Group0059

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0424			1	positive	298.856	299.269	.414
APE0425			1	negative	298.973	299.332	.360
APE0426	COG2246	S	1	positive	299.481	300.602	1.122
APE0427	COG1573	L	1	positive	300.649	301.296	.648
APE0428	COG1750	R	1	negative	301.243	303.153	1.911
APE0429			1	positive	303.244	303.786	.543
APE0430			1	negative	303.403	303.720	.318
APE0431			1	positive	303.833	304.911	1.079
APE0432			1	negative	304.284	304.688	.405
APE0434			1	positive	305.005	305.611	.607
APE0436	COG1093	J	1	negative	305.192	305.941	.750

Group0060

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES015	COG2051	J	1	negative	306.121	306.342	.222
APES016	COG1631	J	1	negative	306.359	306.550	.192
APE0437			1	negative	306.674	308.859	2.186
APE0439			1	positive	307.209	307.841	.633

Group0061

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES017			1	negative	308.989	309.186	.198
APE0442	COG1594	K	1	negative	309.201	309.515	.315
APES018			1	negative	309.642	309.842	.201
APE0443	COG1761	K	1	negative	309.915	310.223	.309
APE0444	COG3286	S	1	negative	310.227	310.832	.606
APE0445	COG1096	J	1	negative	310.912	312.190	1.279

Group0062

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0447	COG1736	J	1	negative	312.215	313.237	1.023
APE0448			1	positive	312.650	313.258	.609

Group0063

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0449	COG0197	J	1	negative	313.378	313.902	.525
APE0450	COG0303	H	1	positive	313.995	315.728	1.734
APE0451			1	negative	314.028	314.714	.687

Group0064

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Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APES019			1	negative	315.792	315.986	.195
APE0452			1	negative	316.237	316.791	.555
APE0453			1	positive	316.247	317.576	1.330
APE0454	COG1489	G	1	negative	316.820	317.542	.723
APE0456			1	negative	317.632	318.099	.468
APE0457	COG0160	E	1	positive	317.638	318.996	1.359

Group0065

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0458		1	negative	318.432	318.914	.483

Group0066

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0459		1	negative	319.335	319.673	.339

Group0067

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0460			1	positive	319.733	320.038	.306
APE0461	COG1591	L	1	positive	320.272	320.703	.432
APE0462	COG1855	R	1	negative	320.700	322.241	1.542
APE0463			1	positive	321.610	322.074	.465
APE0464			1	positive	322.317	323.228	.912
APE0465	COG0301	H	1	negative	323.288	324.526	1.239

Group0068

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0466		1	positive	324.030	324.335	.306

Group0069

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0468			1	positive	324.606	325.049	.444
APE0469	COG1318	K	1	positive	325.141	325.575	.435

Group0070

Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
APE0470	COG1277	R	1	negative	325.980	326.717	.738

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All of the data for the transient connectron 917 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type
                             917 synthetic

Control Sequences - Synthetic Pair of Linked DNA Binding Objects that recognize the sequences G1 = cccgacacaacctgc and G2 = cccgggggttcccgag

Target Sequences - Direction	Chromosome	T1_Id	Start	Stop	Length
negative	1	218	284.071	284.008	.064

		T2_Id	Start	Stop	Length
		295	326.878	326.716	.163

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0053	APE0413	COG0553	positive	284.391	287.510	3.120
2	1	Group0054	APE0414		positive	287.521	291.639	4.118
3	1	Group0054	APE0415	COG1483	negative	291.639	288.073 ,	3.567
4	1	Group0055	APE0416	COG1743	positive	291.643	295.139	3.496
5	1	Group0055	APE0417		positive	292.319	292.636	.318
6	1	Group0055	APE0418		positive	294.690	295.139	.450
7	1	Group0056	tRNA-Thr		positive	295.231	295.529	.298
8	1	Group0056	APES013		positive	295.342	295.518	.177
9	1	Group0057	APES014		positive	295.572	296.676	1.104
10	1	Group0057	APE0419		negative	296.676	295.891	.786
11	1	Group0058	APE0420		positive	297.071	298.857	1.786
12	1	Group0058	APE0422		negative	297.993	297.448	.546
13	1	Group0058	APE0423	COG0084	negative	298.857	298.099	.759
14	1	Group0059	APE0424		positive	298.856	305.941	7.085
15	1	Group0059	APE0425		negative	299.332	298.973	.360
16	1	Group0059	APE0426	COG2246	positive	299.481	300.602	1.122
17	1	Group0059	APE0427	COG1573	positive	300.649	301.296	.648
18	1	Group0059	APE0428	COG1750	negative	303.153	301.243	1.911
19	1	Group0059	APE0429		positive	303.244	303.786	.543
20	1	Group0059	APE0430		negative	303.720	303.403	.318
21	1	Group0059	APE0431		positive	303.833	304.911	1.079
22	1	Group0059	APE0432		negative	304.688	304.284	.405
23	1	Group0059	APE0434		positive	305.005	305.611	.607
24	1	Group0059	APE0436	COG1093	negative	305.941	305.192	.750
25	1	Group0060	APES015	COG2051	positive	306.121	308.859	2.738
26	1	Group0060	APES016	COG1631	negative	306.550	306.359	.192

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27	1	Group0060 APE0437		negative	308.859	306.674	2.186
28	1	Group0060 APE0439		positive	307.209	307.841	.633
29	1	Group0061 APES017		positive	308.989	312.190	3.201
30	1	Group0061 APE0442	COG1594	negative	309.515	309.201	.315
31	1	Group0061 APES018		negative	309.842	309.642	.201
32	1	Group0061 APE0443	COG1761	negative	310.223	309.915	.309
33	1	Group0061 APE0444	COG3286	negative	310.832	310.227	.606
34	1	Group0061 APE0445	COG1096	negative	312.190	310.912	1.279
35	1	Group0062 APE0447	COG1736	positive	312.215	313.258	1.043
36	1	Group0062 APE0448		positive	312.650	313.258	.609
37	1	Group0063 APE0449	COG0197	positive	313.378	315.728	2.350
38	1	Group0063 APE0450	COG0303	positive	313.995	315.728	1.734
39	1	Group0063 APE0451		negative	314.714	314.028	.687
40	1	Group0064 APES019		positive	315.792	318.996	3.204
41	1	Group0064 APE0452		negative	316.791	316.237	.555
42	1	Group0064 APE0453		positive	316.247	317.576	1.330
43	1	Group0064 APE0454	COG1489	negative	317.542	316.820	.723
44	1	Group0064 APE0456		negative	318.099	317.632	.468
45	1	Group0064 APE0457	COG0160	positive	317.638	318.996	1.359
46	1	Group0065 APE0458		positive	318.432	318.914	.483
47	1	Group0066 APE0459		positive	319.335	319.673	.339
48	1	Group0067 APE0460		positive	319.733	324.526	4.793
49	1	Group0067 APE0461	COG1591	positive	320.272	320.703	.432
50	1	Group0067 APE0462	COG1855	negative	322.241	320.700	1.542
51	1	Group0067 APE0463		positive	321.610	322.074	.465
52	1	Group0067 APE0464		positive	322.317	323.228	.912
53	1	Group0067 APE0465	COG0301	negative	324.526	323.288	1.239
54	1	Group0068 APE0466		positive	324.030	324.335	.306
55	1	Group0069 APE0468		positive	324.606	325.575	.969
56	1	Group0069 APE0469	COG1318	positive	325.141	325.575	.435
57	1	Group0070 APE0470	COG1277	positive	325.980	326.717	.738

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	220	positive	284.009	284.071	.063
2	1	221	negative	284.144	284.073	.072
3	1	222	positive	284.073	284.145	.073
4	1	225	negative	284.251	284.158	.094
5	1	226	positive	284.158	284.251	.094
6	1	228	positive	284.253	284.280	.028
7	1	231	positive	284.283	284.305	.023
8	1	240	positive	295.415	295.444	.030
9	1	248	negative	300.757	300.742	.016
10	1	249	negative	300.781	300.767	.015
11	1	253	positive	305.334	305.348	.015
12	1	254	positive	305.358	305.372	.015
13	1	255	negative	305.566	305.552	.015
14	1	257	negative	305.582	305.568	.015

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15	1	273	negative	317.682	317.668	.015
16	1	275	negative	317.704	317.690	.015
17	1	277	positive	319.097	319.127	.031
18	1	283	negative	320.513	320.484	.030
19	1	290	negative	325.979	325.950	.030
20	1	291	positive	325.950	325.979	.030
21	1	294	negative	326.878	326.716	.163

The verbose description of the transient connectron 917 is:

In the Aeropyrum pernix K1 complete genome the synthetic
connectron number 917 is generated by a synthetic pair of linked
DNA binding objects that recognizes the sequences G1 =
cccgacacaacctgc and G2 = cccggggttcccgag. The target sequences
(T1-T2) are on the negative strand of the genomic DNA on
chromosome 1. The identifier number of the initiating target
sequence (T1) is 218. The genomic start and stop positions of
this initiating target sequence are 284.071 KB and 284.008 KB
with a length of 0.064 KB. The identifier number of the
terminating target sequence (T2) is 295. The genomic start and
stop positions of this terminating target sequence are 326.878
KB and 326.716 KB with a length of 0.163 KB.

This connectron controls the modulation of the expression of the
following gene(s): (1) The gene that has the name APE0413 and
with a COG identifier of COG0553. The genomic start and stop
positions of this gene are 284.391 KB and 287.510 KB with a
length of 3.120 KB. (2) The gene that has the name APE0414. The
genomic start and stop positions of this gene are 287.521 KB and
291.639 KB with a length of 4.118 KB. (3) The gene that has the
name APE0415 and with a COG identifier of COG1483. The genomic
start and stop positions of this gene are 291.639 KB and 288.073
KB with a length of 3.567 KB. (4) The gene that has the name

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APE0416 and with a COG identifier of COG1743. The genomic start
and stop positions of this gene are 291.643 KB and 295.139 KB
with a length of 3.496 KB. (5) The gene that has the name
APE0417. The genomic start and stop positions of this gene are
292.319 KB and 292.636 KB with a length of 0.318 KB. (6) The
gene that has the name APE0418. The genomic start and stop
positions of this gene are 294.690 KB and 295.139 KB with a
length of 0.450 KB. (7) The gene that has the name tRNA-Thr.
The genomic start and stop positions of this gene are 295.231 KB
and 295.529 KB with a length of 0.298 KB. (8) The gene that has
the name APES013. The genomic start and stop positions of this
gene are 295.342 KB and 295.518 KB with a length of 0.177 KB.
(9) The gene that has the name APES014. The genomic start and
stop positions of this gene are 295.572 KB and 296.676 KB with a
length of 1.104 KB. (10) The gene that has the name APE0419.
The genomic start and stop positions of this gene are 296.676 KB
and 295.891 KB with a length of 0.786 KB. (11) The gene that has
the name APE0420. The genomic start and stop positions of this
gene are 297.071 KB and 298.857 KB with a length of 1.786 KB.
(12) The gene that has the name APE0422. The genomic start and
stop positions of this gene are 297.993 KB and 297.448 KB with a
length of 0.546 KB. (13) The gene that has the name APE0423 and
with a COG identifier of COG0084. The genomic start and stop
positions of this gene are 298.857 KB and 298.099 KB with a
length of 0.759 KB. (14) The gene that has the name APE0424.
The genomic start and stop positions of this gene are 298.856 KB
and 305.941 KB with a length of 7.085 KB. (15) The gene that has
the name APE0425. The genomic start and stop positions of this
gene are 299.332 KB and 298.973 KB with a length of 0.360 KB.
(16) The gene that has the name APE0426 and with a COG
identifier of COG2246. The genomic start and stop positions of
this gene are 299.481 KB and 300.602 KB with a length of 1.122

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KB. (17) The gene that has the name APE0427 and with a COG identifier of COG1573. The genomic start and stop positions of this gene are 300.649 KB and 301.296 KB with a length of 0.648 KB. (18) The gene that has the name APE0428 and with a COG identifier of COG1750. The genomic start and stop positions of this gene are 303.153 KB and 301.243 KB with a length of 1.911 KB. (19) The gene that has the name APE0429. The genomic start and stop positions of this gene are 303.244 KB and 303.786 KB with a length of 0.543 KB. (20) The gene that has the name APE0430. The genomic start and stop positions of this gene are 303.720 KB and 303.403 KB with a length of 0.318 KB. (21) The gene that has the name APE0431. The genomic start and stop positions of this gene are 303.833 KB and 304.911 KB with a length of 1.079 KB. (22) The gene that has the name APE0432. The genomic start and stop positions of this gene are 304.688 KB and 304.284 KB with a length of 0.405 KB. (23) The gene that has the name APE0434. The genomic start and stop positions of this gene are 305.005 KB and 305.611 KB with a length of 0.607 KB. (24) The gene that has the name APE0436 and with a COG identifier of COG1093. The genomic start and stop positions of this gene are 305.941 KB and 305.192 KB with a length of 0.750 KB. (25) The gene that has the name APES015 and with a COG identifier of COG2051. The genomic start and stop positions of this gene are 306.121 KB and 308.859 KB with a length of 2.738 KB. (26) The gene that has the name APES016 and with a COG identifier of COG1631. The genomic start and stop positions of this gene are 306.550 KB and 306.359 KB with a length of 0.192 KB. (27) The gene that has the name APE0437. The genomic start and stop positions of this gene are 308.859 KB and 306.674 KB with a length of 2.186 KB. (28) The gene that has the name APE0439. The genomic start and stop positions of this gene are 307.209 KB and 307.841 KB with a length of 0.633 KB. (29) The

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gene that has the name APES017. The genomic start and stop
positions of this gene are 308.989 KB and 312.190 KB with a
length of 3.201 KB. (30) The gene that has the name APE0442 and
with a COG identifier of COG1594. The genomic start and stop
5   positions of this gene are 309.515 KB and 309.201 KB with a
length of 0.315 KB. (31) The gene that has the name APES018.
The genomic start and stop positions of this gene are 309.842 KB
and 309.642 KB with a length of 0.201 KB. (32) The gene that has
the name APE0443 and with a COG identifier of COG1761. The
10   genomic start and stop positions of this gene are 310.223 KB and
309.915 KB with a length of 0.309 KB. (33) The gene that has the
name APE0444 and with a COG identifier of COG3286. The genomic
start and stop positions of this gene are 310.832 KB and 310.227
KB with a length of 0.606 KB. (34) The gene that has the name
15   APE0445 and with a COG identifier of COG1096. The genomic start
and stop positions of this gene are 312.190 KB and 310.912 KB
with a length of 1.279 KB. (35) The gene that has the name
APE0447 and with a COG identifier of COG1736. The genomic start
and stop positions of this gene are 312.215 KB and 313.258 KB
20   with a length of 1.043 KB. (36) The gene that has the name
APE0448. The genomic start and stop positions of this gene are
312.650 KB and 313.258 KB with a length of 0.609 KB. (37) The
gene that has the name APE0449 and with a COG identifier of
COG0197. The genomic start and stop positions of this gene are
25   313.378 KB and 315.728 KB with a length of 2.350 KB. (38) The
gene that has the name APE0450 and with a COG identifier of
COG0303. The genomic start and stop positions of this gene are
313.995 KB and 315.728 KB with a length of 1.734 KB. (39) The
gene that has the name APE0451. The genomic start and stop
30   positions of this gene are 314.714 KB and 314.028 KB with a
length of 0.687 KB. (40) The gene that has the name APES019.
The genomic start and stop positions of this gene are 315.792 KB

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and 318.996 KB with a length of 3.204 KB. (41) The gene that has the name APE0452. The genomic start and stop positions of this gene are 316.791 KB and 316.237 KB with a length of 0.555 KB. (42) The gene that has the name APE0453. The genomic start and stop positions of this gene are 316.247 KB and 317.576 KB with a length of 1.330 KB. (43) The gene that has the name APE0454 and with a COG identifier of COG1489. The genomic start and stop positions of this gene are 317.542 KB and 316.820 KB with a length of 0.723 KB. (44) The gene that has the name APE0456. The genomic start and stop positions of this gene are 318.099 KB and 317.632 KB with a length of 0.468 KB. (45) The gene that has the name APE0457 and with a COG identifier of COG0160. The genomic start and stop positions of this gene are 317.638 KB and 318.996 KB with a length of 1.359 KB. (46) The gene that has the name APE0458. The genomic start and stop positions of this gene are 318.432 KB and 318.914 KB with a length of 0.483 KB. (47) The gene that has the name APE0459. The genomic start and stop positions of this gene are 319.335 KB and 319.673 KB with a length of 0.339 KB. (48) The gene that has the name APE0460. The genomic start and stop positions of this gene are 319.733 KB and 324.526 KB with a length of 4.793 KB. (49) The gene that has the name APE0461 and with a COG identifier of COG1591. The genomic start and stop positions of this gene are 320.272 KB and 320.703 KB with a length of 0.432 KB. (50) The gene that has the name APE0462 and with a COG identifier of COG1855. The genomic start and stop positions of this gene are 322.241 KB and 320.700 KB with a length of 1.542 KB. (51) The gene that has the name APE0463. The genomic start and stop positions of this gene are 321.610 KB and 322.074 KB with a length of 0.465 KB. (52) The gene that has the name APE0464. The genomic start and stop positions of this gene are 322.317 KB and 323.228 KB with a length of 0.912 KB. (53) The gene that has the name APE0465 and

with a COG identifier of COG0301. The genomic start and stop
positions of this gene are 324.526 KB and 323.288 KB with a
length of 1.239 KB. (54) The gene that has the name APE0466.
The genomic start and stop positions of this gene are 324.030 KB
and 324.335 KB with a length of 0.306 KB. (55) The gene that has
the name APE0468. The genomic start and stop positions of this
gene are 324.606 KB and 325.575 KB with a length of 0.969 KB.
(56) The gene that has the name APE0469 and with a COG
identifier of COG1318. The genomic start and stop positions of
this gene are 325.141 KB and 325.575 KB with a length of 0.435
KB. (57) The gene that has the name APE0470 and with a COG
identifier of COG1277. The genomic start and stop positions of
this gene are 325.980 KB and 326.717 KB with a length of 0.738
KB.

This connectron controls the turning off of the expression of
the following connectron(s): (1) The connectron that has the
identifier 220 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 284.009
KB and 284.071 KB with a length of 0.063 KB. (2) The connectron
that has the identifier 221 is on chromosome 1 in the negative
direction. The genomic start and stop positions of this
connectron are 284.144 KB and 284.073 KB with a length of 0.072
KB. (3) The connectron that has the identifier 222 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 284.073 KB and 284.145 KB
with a length of 0.073 KB. (4) The connectron that has the
identifier 225 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 284.251
KB and 284.158 KB with a length of 0.094 KB. (5) The connectron
that has the identifier 226 is on chromosome 1 in the positive
direction. The genomic start and stop positions of this

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connectron are 284.158 KB and 284.251 KB with a length of 0.094
KB. (6) The connectron that has the identifier 228 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 284.253 KB and 284.280 KB

5   with a length of 0.028 KB. (7) The connectron that has the
identifier 231 is on chromosome 1 in the positive direction. The
genomic start and stop positions of this connectron are 284.283
KB and 284.305 KB with a length of 0.023 KB. (8) The connectron
that has the identifier 240 is on chromosome 1 in the positive

10   direction. The genomic start and stop positions of this
connectron are 295.415 KB and 295.444 KB with a length of 0.030
KB. (9) The connectron that has the identifier 248 is on
chromosome 1 in the negative direction. The genomic start and
stop positions of this connectron are 300.757 KB and 300.742 KB

15   with a length of 0.016 KB. (10) The connectron that has the
identifier 249 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 300.781
KB and 300.767 KB with a length of 0.015 KB. (11) The connectron
that has the identifier 253 is on chromosome 1 in the positive

20   direction. The genomic start and stop positions of this
connectron are 305.334 KB and 305.348 KB with a length of 0.015
KB. (12) The connectron that has the identifier 254 is on
chromosome 1 in the positive direction. The genomic start and
stop positions of this connectron are 305.358 KB and 305.372 KB

25   with a length of 0.015 KB. (13) The connectron that has the
identifier 255 is on chromosome 1 in the negative direction. The
genomic start and stop positions of this connectron are 305.566
KB and 305.552 KB with a length of 0.015 KB. (14) The connectron
that has the identifier 257 is on chromosome 1 in the negative

30   direction. The genomic start and stop positions of this
connectron are 305.582 KB and 305.568 KB with a length of 0.015
KB. (15) The connectron that has the identifier 273 is on

chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 317.682 KB and 317.668 KB with a length of 0.015 KB. (16) The connectron that has the identifier 275 is on chromosome 1 in the negative direction. The

5   genomic start and stop positions of this connectron are 317.704 KB and 317.690 KB with a length of 0.015 KB. (17) The connectron that has the identifier 277 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 319.097 KB and 319.127 KB with a length of 0.031

10   KB. (18) The connectron that has the identifier 283 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 320.513 KB and 320.484 KB with a length of 0.030 KB. (19) The connectron that has the identifier 290 is on chromosome 1 in the negative direction. The

15   genomic start and stop positions of this connectron are 325.979 KB and 325.950 KB with a length of 0.030 KB. (20) The connectron that has the identifier 291 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 325.950 KB and 325.979 KB with a length of 0.030

20   KB. (21) The connectron that has the identifier 294 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 326.878 KB and 326.716 KB with a length of 0.163 KB.

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